OM protein protein search, using sw model

Run on: May 18, 2002, 05:20:10 ; Search time 58.31 Seconds (without alignments)
1919.809 Million cell updates/sec

Title: Perfect score: Sequence:

Scoring table: US-08-779-457-2 6254 1 MICQKFCVVLLHWEFIYVIT......QTCSTQTHKIMENKMCDLTV 1165

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	æ	7	6	ر ت	4	ω	2	μ.	No.	Result
166	166.5	69.	170	172	174	177	182.5	188	191.5	209.5	220	251.5	277	281.5	284	288.5	294.5	313	339.5	345.5	366	3340	3729	3785	3785	3793	4766.5	4784.5	Score	
2.7	2.7	2.7	2.7	2.8	2.8	2.8	2.9	3.0	μ. μ	<u>ω</u> .ω	3.5	4.0	4.4	4.5	4.5	4.6	4.7	5.0			5.9	ω.	59.6		9	0	Φ	6	Match:	Query
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hypothetical prote	tyr	neogenin – chicken	neural cell adhesi		"	fibronectin - Afri	Ö		titin - rabbit (fr	prolactin receptor	n recepto	protein-tyrosine-p	granulocyte colony	differentiation-st	granulocyte colony	granulocyte colony	leukemia inhibitor	granulocyte colony	interleukin-6 sign	membrane glycoprot	ч	receptor,		receptor,	receptor,		receptor,	leptin receptor, O	Description	

F;861-1162/Domain: intracellular #status p

redicted <INT>

Query Match Best Local Similarity

76.5%; 75.6%;

Score 478 Pred. No.

84.5; DB 2; Length 1162; . 6.5e-303;

4	4	4	4	41	4	ω	ω	ω	ω	ω	·ω	w	ω	ω	ω	
5 148.5	_	3 150.5		_	0 153.5	9 153.5	8 154.5	7 156	6 158	5 158	4 158	3 159	2 160	1 165	0 · 165	
2.4	2.4	2.4	2.4	2.5	2.5	2.5	2.5	2.5	2.5	2.5	2.5	N .5	2.6	2.6	2.6	
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ALIGNMENTS

RESULT

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A;Gene: Ia C;Keywords: appetite; transmembrane protein F;840-860/Domain: transmembrane #status predicted <tmk></tmk>
Experimental source: adipose cell . Comment: This receptor is obese-phenotype-linked mutant, found in Genetics:
A; Molecule type: mRNA A; Residues: 1-889, 'RADTL' <ii2> A; Cross-references: DDBJ:D84125; NID:g1374707; PIDN:BAA: 2230.1; PID:g1374708</ii2>
A;Title: Phenotype-linked animo acid.alteration in reptin receptor conversion zucker in A;Reference number: JC4797; MUID:96212906 A;Accession: JC4797
Tida, M.; Murakami, T.; Ishida, K.; Mizuno, A.; Kuwajima, M.; Shima, K. lochem. Biophys. Res. Commun. 222, 19-26, 1996
A;Molecule type: MKNA A;Residues: 840-1162 <iid> A:Cross-references: DDRT:D84550</iid>
Accession: PC4184
n at codo
R;Iida, M.; Murakami, T.; Ishida, K.; Mizuno, A.; Kuwajima, M.; Shima, K. Biochem. Biophys. Res. Commun. 224, 597-604, 1996
Cross-references: DDBJ:D85559
A;Molecule type: mRNA A;Residues: 1-796,'G',1157-1158,'TVLLLN'. <ta3></ta3>
A; Status: preliminary
A;Residues: 1-889,'RADTL' <ta2> A:Cross-references: DDBJ:D85557</ta2>
Molecule type: mRNA
A;Status: preliminary
A;Cross-references: DDBJ:D85558; NID:g1526441; PIDN:BAA12831.1; PID:d1013515; PID:g15
A;Reference number: JC4895; MUID:96332408 A;Accession: JC4895
Molecular cloning of rat leptin re
R;Takaya, K.; Ogawa, Y.; Isse, N.; Okazaki, T.; Satoh, N.; Masuzaki, H.; Mori, K.; Ta Riochem Biophys Res Commun 225 75-R1 1996
;Accession: JC4895; JC4896; JC4897; PC4184; JC4797
C:Species: Rattus norvegicus (Norway rat)
leptin receptor, Ob-Rb - rat
BC4184

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RESULT 2

S68438

leptin receptor, splice form Ob-Rb - mouse
C;Species: Mus musculus (house mouse)
C;Species: Musculus (house mouse)
C;Species: Musculus (house mouse)
C;Species: Musculus (house mouse)
C;Species: Musculus (house mouse)
R;Lee, G,H; Proenca, R; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;
R;Lee, G,H; Proenca, R; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;
R;Lee, G,H; Proenca, R; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;
R;Lee, G,H; Proenca, R; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;
R;Lee, G,H; Proenca, R; Monte; Mull: S6231997
A;Cross-references: EMBL: U49107; NID: 91195486; PIDN: AAC52421.1; PID: 91195487
A;Cross-references: EMBL: U49107; NID: 91195486; PIDN: AAC52421.1; PID: 91195487
A;Cross-references: EMBL: U49107; NID: 91195486; PIDN: AAC52421.1; PID: 91195487
A;Cross-references: EMBL: U49107; NID: 91195486; PIDN: AAC52421.1; PID: 91195487
A;Cross-references: EMBL: U49107; NID: 91195486; PIDN: AAC52421.1; PID: 91195487
A;Cross-references: EMBL: U49107; NID: 91195486; PIDN: AAC52424.1; PID: 91195487
A;Cross-references: EMBL: U49107; NID: 91195492; PIDN: AAC52424.1; PID: 91195493
A;Cross-references: EMBL: U4910; NID: 91195492; PIDN: AAC52424.1; PID: 91195493
A;Cross-references: EMBL: U4910; NID: 91195492; PIDN: AAC52424.1; PID: 91195493
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NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
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879; Conserv
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RESULT 3
S68440
Leptin receptor, splice form Ob-Rd - mouse
C; Species: Mus musculus (house mouse)
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #to
C; Accession: S68440
R; Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.;
Nature 379, 632-635, 1996
A; Title: Abnormal splicing of the leptin receptor in of
A; Reference number: S68437; MUID:96231997
A; Accession: S68440
A; Status: nucleic acid sequence not shown; translation
A; Molecule type: mRNA
A; Residues: 1-900 < LEE>
A; Cross-references: EMBL:U49109; NID:g1195490; PIDN:AJ
A; Experimental source: tissue hypothalamus
A; Note: the nucleotide sequence was submitted to the I
C; Comment: For alternative splice forms, see PIR:S684:
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RESULT S68439 leptin

receptor,

splice

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mouse

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A;Gene: Ob-Rd
C;Keywords: alternative splicing;
F;840-860/Domain: transmembrane #
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Pred. No.
3; Mismat
  7IRINHSLGSLDSPPTCVLPDSVVKPLPP 540
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1.4e-238;
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C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-2000 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
C:Accession: 568439; 568441
R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; Fr.
R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; Fr.
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Local Similarity 77.3%;
es 689; Conservative 81
                                        SNVKAEITVNTGLLKVSWEKPVFPENNLQFQIRYGLSGKEIQWKTHEVFDAKSKSASLLV
                                                          SSVKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV
                                                                                                                    PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV
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Pred. No. 4.5e-238;
81; Mismatches 119;
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FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP 240

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leptin receptor, splice form Ob-Ra - mouse
C; Species: Mus musculus (house mouse)
C; Date: 31-Dec-2000 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
C; Date: 31-Dec-2000 #sequence 7.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;
R; Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;
Nature 379, 632-635, 1996
A; Title: Abnormal splicing of the leptin receptor in diabetic mice.
A; Reference number: S68437; MUID:96231997
A; Reference number: S68437; MUID:96231997
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: mRNA
A; Residues: 1-894 <LEE>
A; Cross: references: EMBL:U49106; NID:g1195484; PIDN:AAC52420.1; PID:g1195485
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C; Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:
C; Genetics:
A; Gene: Ob-Ra
C; Keywords: alternative splicing; appetite
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                                                                                   MMCQKFYVVLLHWEFLYVIAALNLAYPISPWKFKLFCGPPNTTDDSFLSPAGAPNNASAL
                                                                                                          MICQKECVVLLHWEEIYVITAFNLSYPITPW
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                                                                                                                                                                   689; Conservative
                                                                                                                                                                                         60.5%;
77.3%;
                                                                                                                                                                      81;
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Pred. No.
                                                                                                                                                                   ore 3785; DB 2;
ed. No. 4.6e-238;
Mismatches 119;
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J.I.;

1996 PIR:

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RESULT 6
$74225

Leptin receptor, isoform Ob-Rf - rat
C; Species: Rattus norvegicus (Norway rat)
C; Date: 29-Jan-1998 #sequence_revision 13-F6
C; Accession: $74225
R; Wang, M.Y.; Zhou, Y.T.; Newgard, C.B.; Uncertain for the company of the company
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-895 <WAN>
A;Cross-references: EMBL:U53144; NID:g1395212;
A;Experimental source: strain Sprague-Dawley; 1
C;Genetics:
A;Gene: rOb-R
C;Keywords: appetite; transmembrane protein
F;840-860/Domain: transmembrane #status predict
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                                          ROLGVNWDIECWMKGDLTLFICHMEPLLKNPFKNYDSKVHLLYDLPEVIDDLPLPPLKDS
                                                                                                                           KGASEALVEAKFNSTGIYVSELSKTIFHCCFGNEQGQNCSALTGNTEGKTLASVVKPLVF
FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP
                                                                 QQIDANWNIQCWLKGDLKLFICYVESLFKNLFRNYNYKVHLLYVLPEVLEDSPLVPQKGS
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larity 76.5%;
Conservative
                                                                                                                                                                                                                                                                                                                Score 3729; DB 2;
Pred. No. 2e-234;
84; Mismatches 123;
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A; Reference number: $68437; MUID:96231997
A; Accession: $68441
A; Status: nucleic acid sequence not shown; tr
A; Molecule type: mRNA
A; Residues: 1-805 < LEE>
A; Cross-references: EMBL:U49110; NID:g1195492
A; Experimental source: splice form Re; tissue
A; Note: the nucleotide sequence was submitted
C; Comment: For alternative splice forms, see
C; Genetics:
A; Gene: Ob-Re
C; Keywords: alternative splicing; appetite
                                                                                                                                                      leptin receptor, splice form Ob-Re - mous C; Species: Mus musculus (house mouse) C; Date: 31-Dec-2000 #sequence_revision 31 C; Accession: $68441 R; Lee, G.H.; Proenca, R.; Montez, J.M.; C Nature 379, 632-635, 1996 A; Title: Abnormal splicing of the leptin A; Reference number: $68437; MUID: 96231997
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                                            35492; PIDN:AAC52424.1; PID:g1195493 issue hypothalamis ltted to the EMBL Data Library, February 1996 see PIR:S68437, PIR:S68438, PIR:S68439, PIR:
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Length 805;

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RESULT 8
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glycoprotein 130 - mouse
C; Species: Mus musculus (house mouse)
C; Date: 02-Aug-1996 #sequence_revision 02-Aug
C; Accession: I49699; I48370
R; Saito, M.; Yoshida, K.; Hibi, M.; Taga, T.;
J. Immunol. 148, 4066-4071, 1992
A; Title: Molecular cloning of a murine IL-6 1
A; Reference number: I48370; MUID:92291532
A; Accession: I49699
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-917, <RES>
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A;Accession: I48370
A;Status: translated from GB/EMBL/
A;Molecule type: mRNA
A;Residues: 1-917 <RE2>
A;Cross-references: EMBL:X62646; N
C;Genetics:
A;Gene: gp130
C;Superfamily: cytokine receptor h
C;Keywords: glycoprotein
F;134-314/Domain: cytokine recepto
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Best Local Similarity 20.9%;
Matches 191; Conservative 140
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                                                                       QGEIEAIVVPVCLAFLLTTLLGVLFCFNKRD
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VTPVFATGPGGSESLKAYLKQAAPARGPTVR
                                                                                                                                                                   VDKVKPTPPYNLSYTNSEELSSILKLSW---
                                                                                                                                                                                                                  DVGNHTKFTFLWTEQAHTVTVLAINSIGASV
                                                                                                                                                                                                                                   DR-PSRPPSFWYKTNPSHGQEYRSVRLIWKA
                                                                                                                                                                                                                                                  IKVPMRGPEFWRI INGDTMKKEKNVTLLWKP
                                                                                                                                                                                                                                                                                                                                                                                            ASYIVWKTNHA-AVPREQUTVINRTTSSVTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                           STPRVFTTQDVIYF ---
          STEGHSSGIGGSSCMSSSRPSISSNE
                                                                                                       ISYRTSYCKEMYVHYDSSHTEYTLSSLSSDT
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                                         -RHNFNSKDQMYSDGNF
                                                                                                                                                                                                                                                                         -WKMYEVYDAKSKSVSLPVPDL--CAV
                                                                                 VIVPVIISSSI-LLLGTLLISHQR-
                                                                                                                 VGKPKII---NSFTQDDIEKHQSDAGLY-----
                         GSVCISDQFNSVNFSEAEGTE
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NID: g19359
                                                                                                        1; PIDN:AAA37723.1; PID:g193592
816; PIDN:CAA44515.1; PID:g840817
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42;

DSVVKPLPPSSVKAEITINI-GLLKISWEKPVFPENNLQFQIRYGLSG-----KEVQ--- 582 ---TGTELTVNLTNDRYVASLAARNKVGKSAAAV-LTIPSPHVTAAYSVVNLKAFP-KDN 435 FEHLFIKHTASVTCGPLLLEPETISEDISVDTSWKNKDEMMPTTVVSLLSTTDLEK-----KFPDC--QSKHGTSCMVSYMPTYYVN-IEVWVEAENALGKVSSESINFDP 214 Score 366; DB 2; Length 917; Pred. No. 1.2e-15; Nismatches 338; Indels 244; Gaps -MKKLFWEDVPNPKNCSWAQGLNFQKPET TKKVGKNEAVLAWDQIPVDDQNGFIRNYS 553 LMKNDSLCSVQRY--VINHHTSCNGTWSE 693 YVFRIRSIKDSGKGYWSDWSEEASGTTYE MTCRWSTSTIQSLAESTLQLRYHRSSLYC 473 TDV--VLPSVQLT-----CNILSFGQIE 112 PEFPVVQRGSNFTAICVLKEACLQHYYVN 61 PPKILTSVGSNVSFHCIYKK---ENKIVP 362 VTYEDESQRQ--PFVKYATLISNSKPSET 998 EIEANNKKPCPDD----LKSVDLFKKEKV LIKKHIWPNVPDPSKSHIAQWSPHTPP---LYMVRMAAYTDEGGKDGPEFTFTTPKFA 612 VEDWQQEDATVNRTHLRGRLLESKCYQIT 493 --KWLRISSSVKKYYIHDHFIPIEKYQFS 810 ANFNLTESWP-MSKVNIVQSLSAYPLNSS 752 LPLSEANGKILDYEVILTQSKSVSQTYTV 380 YAVQVRCKRLDGLGYWSNWSNPAYTVVMD 635 FNLNETKPRGKFTYDAVYCCNEHECHHRY 422 --ENESAQSTASTVEYSTVVHSGYRHQV 769 ------VSSGLGGLLDLKSDIQYRT Length 917; 950 894 670 321 843 818

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membrane glycoprotein gp130 precursor - human C; Species: Homo sapiens (man) C; Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 28-Jul-2 C; Accession: A36337 R; Hibi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T. Cell 63, 1149-1157, 1990 A; Title: Molecular cloning and expression of an IL-6 signal transducer, A; Reference number: A36337; MUID: 91084844 A; Accession: A36337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 5q11-5q11
C; Superfamily: cytokine receptor homology
C; Keywords: glycoprotein; membrane protein
F; 134-316/Domain: cytokine receptor homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M57230; LC;Genetics:
A;Gene: GDB:IL6ST; GP130
A;Cross-references: GDB:126725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-918 <HIB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92
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                                                                                                                                                               SLCSVQRYVINHHTSCNGTWSEDVGNH----TKFTFLWTEQAHTVTVLAINSIGASVANF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FNLNETKPRGKFTYDAVYCCNEHECHHRYAELYVIDV------NINISC-ETDGYLTK 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FERSNOV--LSGN 839
NLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNEDGE--IKW
                                                                                                                                                                                                                                     RCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNVTLLWKPLMKND
                                                                                                                                                                                                                                                                                        TNPSIKSVIILKYNIQYRTKDAST-----WSQIPPEDTASTRSSFTVQDLKPFTEYVFRI
                                                                                                                                                                                                                                                                                                                                                               VYFVN-IEVWVEAENALGKVTSDHINFDPVYKVKPNPPHNLS---VINSEELSSILKLTW
                                                                                                                                                                                                                                                                                                                                                                                                                                 PESPVVQLHSNFTAVCVLKEKCMDYFHVNANYIVWKTN-HFTIPKEQYTIINRTASSVTF
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                                    LRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKII--
                                                                                                                                                                                                                  RCMKEDGKGYWSDWSEEASGITYEDR-PSKAPSFWYKIDPSHTQGYRTVQLVWKTLPPFE
                                                                                                                                                                                                                                                                                                               EKP----VFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPVPDL--CAVYAVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIHPISEPKDCYLQSDGFYECI--FQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEEQGLINSSYTK-CFSSKNSP----LKDSFSNSSWEIEAQAFFILSDQHPNIISPHLTF
                                                                        LTIPACDFQATHPVMDLKAFP-KDNMLWVEWTTPRESVK--KYILEWCVLSDKAPCITDW
                                                                                                                                               ANGKILDYEVT --
                                                                                                                                                                                                                                                                                                                                                                                                  IFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPPSSVKAEITIN----IGLLKISW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPKILTSVGSNVSFHCIYKK---ENKIVPSKEIVWWMNLAEKIPQSQYDVVSDHVSKVTF 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --ASLNIQLTCNILTFGQLEQNVYGITIISGLPPEKPKNLSCIVNEG--KK
                                                                                                                                            --LTRWKSHLQNYTVNATKLTVNLTNDRYLATLTVRNLVGKSDAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.5%;
19.8%;
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%; Pred. No. 2.6e-14;
119; Mismatches 305;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          918;
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Qγ	826
Дb	531 GKNEAVLEWDQLPVDVQNGFIRNYTIFYRTIIGNETAVNVDSSHTEYTLSSLTSDT-LYM 589
Qу	PVIISSSI-LLLGTLLIS
ДЪ	590 VRMAAYTDEGGKDGPEFTETTPKFAQGEIEAIVVPVCLAFLLTTLLGVLFCFNKRDLIKK 649
Qy	70 LFWEDVPNPKNCSWAQGLNFQKPETFEHLF KHTASVTCGPLLLEPETISEDISVDT
) <u>[</u>	NAME ENCOCONTRACTOR NECESTATION OF THE TRACTOR OF THE TRACTOR OF THE OCCUPANT OF THE OCCUP
B 2	678 SKDQMYSDGNFTDVSVVEIEANDKKPFPEDLKS 710
Qy	987 ATLISNSKPSETGEEQGLINSSVTKCFSSKNSPLKDSFSNSS 1028
Дb	
RESUI A4425	10
C;Spec C;Date	3.0
R; Wang, 1	y, Y.; Nesbitt
A; Tit A; Ref	Molecular clonin nce number: A4425
MO St	: prelimi le type:
A;Resid A;Exper	idues: 1-918 <wan> erimental source: liver</wan>
A; Note: C; Super C; Keywo F; 134-3	e: sequence extrac erfamily: cytokine words: transmembra -315/Domain: cytok
Que Bes Mat	5.4%; Score 339.5; DB 2; Length 918; it Local Similarity 20.8%; Pred. No. 6.3e-14; ches 185; Conservative 141; Mismatches 326; Indels 237; Gaps 40;
Qу	[QDVIYFPPKILTSVGSNVSFHCIYKKENKIVPSKEIVWWM
DЪ	14 IFLTTESIGQLVEPCGYIYPEFPVVQRGSNFTATCVLKEKCLQVYSVNATYIVWKTNHV- 72
Qy	2SQYDVVSDHVSKVTFFNLNETKPRGKFTYDAVYCCNEHECHE : ::
망	PKEQVTVINRTASSVTFTDVVFQNVQLTCNILSFGQIEQNVYGIT
Qy	429DVNINISC-ETDGYLTKMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIH 480
Db	IPTNLSCIVNEGKNMLCQLDPGRETYLETNYILKSEWATE
D 0 y	481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINESLGSLDSPPTCYLPDSVVKPL 538 : : : : : :: : :
Qy	LKISWEKPVFPENNLQ
DЪ	PHNLSVTNSEELSSIL
P &	593 SKSVSLPVPDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIIN 650
QY	651 GDTMKKEKNVTLLWKPLMKNDSLCSVQRY VINHHTSCNGTWSEDVGNHTKFTFLWTEQ 708
D.	337 ANHPQEYRSARLIWKTLPLSEANGKILDYEVVLTQSKSVSQTYTVNGTELIVNLTNN 393

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1.7%; Score 294.5; DB 2; Length 1097; al Similarity 19.2%; Pred. No. 7e-11; 215; Conservative 179; Mismatches 385; Indels 339; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       inhibitory factor receptor - human
: Homo sapiens (man)
2-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
on: S17308
on: S17308
D.P.; Thut, C.J.; VandenBos, T.; Gimpel, S.D.; Delaney, P.B.; King, J.; Pr
D. 2839-2848, 1991
Ceukemia inhibitory factor receptor is structurally related to the IL-6 sign ce number: S17308; MUID:92007727
on: S17308
                                                                                                                                                                                                                                                                                preliminary
type: mRNA
: 1-1097 <GEA>
ferences: GB:X61615; NID:g34365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLOVHGVEE----OGGF 837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPLLLEPETISEDISVDTSWKNKDEMMPTTVVSLLSTTDLEKGSVCIS-DQFNSVNFS-- 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AHTVTVLAINSIGASVANENLTFSWPMSKVNIVQSLSAYPLNSSCVIVSW---ILSPSDY 765
                                                            LLYVLPEVLEDSPLVPQKGSFQMVHC------NCS-----VHECC----- 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLINSSVTKCFSSKNSPLKDSFSNSSWEIEAQAFFILSDQHPN----IISPHLTFS--- 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALVQAYVLQGDPREIS----NQSQP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCLWLSW-KPWKPSEYMEQECELRYQPQLKGANWTL--VFHLPSSKDQF---ELCGLHQA 301
  --OSNAÖNWTÄTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----EGLDELLKLEGNE 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVTLNISLHDFYLKHLEPÄSLYHVYLMATSRAGSTNSTGLTLRTLDPSDLNIFLGILCLV 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVNVYTFAGERAPPHAPALHLKHVGTTWAQLEWVPEAPRLGMIPLTHYTIFWADAGDHSF 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PKIINSFT-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQNVTLVAYNKAGTSSPT---TVVFLENEGPAVTGLHAMAQDLNTIWVDWEAPSLLPQGY 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYYTLQMRCIRSSLPGFWSPWS-PG----LQLRPTMKAP----TIRLDTWCQKKQLDPGT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -PTIMTEET----FQLPSFW-----DSSVPSITKITELEEDKKPTHWDSESSGNGSLP 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -NYTLLWKPLMKNDSLCSVQRYVINHHTS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----EAEGTEVTYEDESQRQPFVKYATLISNSKPSETGEE------Q 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----ODDIEKHQSDAGLY------
-- KKGAPHDLKCVTNNLQVWNCSWKAPSGTGRGTDYEVCIENRSRS 89
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                                                                                                                                                                                                                                                                                       PIDN:CAA43805.1; PID:g34366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKFTYDAVYCCNEHECHHRYAELYVIDVNINISCETDGYLTKMTCRWSTSTIQSLA---E
                                                                                                                                                LEPETISEDISVDTSWKNKDEMMPTTVVSLLSTTDLEKGSVC---ISDQFNSVNFSEAEG
                                                                                                                                                                                                                                                                                                  DIPVEELRGFLRGYLFYFGKGERDTSKMRVLESGRSDIKVKNITDISQKTLRIADLQGKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GT---NVVFTTEDNIFGTVIFAGYPPDTPQQLNCETHD-LKEIICSWNPGRVTALVGPRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNVSFHCIYKKENKIVPSKEIVWWMNLAEKIPQSQYDVV---SDHVSKVTFFNLNETKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WASDMPLECATHFVETRCYIDNLHFSGLEEWSDWSPVKNISWIPDSQTKVFPQDKVILVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STSTLYLKWNDRGSV-FPHRSNVIW---EIKVLRKESMELVKLVTHNTTLNGKDTLHHWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDGNLKISWSSPPLVPFPLQYQVKYSENSTTVIR----EADKIVSATSLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYQLEKTSIKIPALSHGDYEITINSLHDFGSSTSKFTLNEQNVSLI-PDTPEILNLSADF
                                                           TAQVIYIDVQSMYQP
                                                                                      T-EVTYED-ESQRQPFVKYATLISNSKPSETGEEQGL-
                                                                                                                      EDTEIIS---PVAERPEDRSDAEPENHVVV--
                                                                                                                                                                              KETFYPDIPNPENC---KALQFQKSVCEGSSALKTLEMNPCTPNNVEVLETRSAF--PKI
                                                                                                                                                                                               KKLFWEDVPNPKNCSWAQGLNFQK--
                                                                                                                                                                                                                                         SYHLVLRAYIDGGVGPEKSMYVVTKENSVGLIIAILIPVAVAVIVGVVTSILCYRKREWI
                                                                                                                                                                                                                                                                                                                                                             IESDEFRPGIRYNFFLYGCRNQGYQLLRSMIGYIEELAPIVAPNFTVEDTSADSILVKWE
                                                                                                                                                                                                                                                                                                                                                                                           YIHDHFIPIEKYQFSLYPIFMEG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSSDEETQSLSEIPDPQHKAEIRLDKNDYIISVVAKNSVGSSPPSKIASMEIPNDDLKIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLQFQIRYGLSGKEYQWKMYEYYDAKSKSYSLPYPDLCAVYAYQYRCKRLDGLGYWSNWS
 EDLDKTAGYRPQANVNTW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -VDSILPGSSYEVQVR----GKRLDGPGIWSDWSTPRVFT---TQDVIYFPPKILTSVG
                            SKNSPLKDSFSNSSWEIEAQAFFILSDQHPNIISP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPPLGLHMEIT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TWSEDVGNHTKFTFLWTEQAHTVTVLAINSIGASVANFNLTFSWPMSKVNIV
                                                                                                                                                                                                                                                                                                                                                                                                                      GKGILLTWHYDPNWTCDY----VIKWCNSSRSEPCLMDWRKVPSNSTETV
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                                                                                                                                                                                                                                                                        AGLYVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -NSSYLVALDKLNPYTLYTFRIRCS-TETFWKWSKWS
                                                          QAKPEEEQENDPVGGAGYKPQMHLPINSTVEDIAAE
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 ASATN
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                                                                                                                     -SYCPPIIEEEIPNPAADEAGG
1042
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                                                                                       INSSVTKCFS-
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LTSVGSNVSFHCIYKKE-NKIVPSKEIVWWMNL

IVHLGDPITASCIIKQNCSHLDPEPQILWRLG

-AELQPGGRQQRLSDGTQESIITLPHLN 93

-- VNINISCETDGYLTKMT 446

AEKIPQSQYDVVSD--HVSKVTFFNLN 397

Indels 219;

Gaps

38;

Matches

156;

125;

Similarity

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398

ETKPRGKFTYDAVYCCNEHECHHRYAELYVID

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granulocyte colony-stimulating factor receptor N; Contains: granulocyte colony-stimulating fac C; Species: Homo sapiens (man)
C; Date: 14-Jun-1991 #sequence_revision 30-Jan-C; Accession: C38252; A38252; JH0330; A46486; SR; Fukunaga, R.; Seto, Y.; Mizushima, S.; Nagat Proc. Natl. Acad. Sci. U.S.A. 87, 8702-8706, 1A; Title: Three different mRNAs encoding human A; Reference number: A38252; MUID:91062348
A; Accession: C38252
A; Status: preliminary
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A; Residues: 1-863 <FUK>
A; Cross-references: GB:M59820; GB
A; Cross-references: pHG11 and pHG5
A; Accession: A38252
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-680,708-863 <FU2>
A; Cross-references: GB:M59818; GB
A; Note: Clone pHO3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminal A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 855-863 <SET>
A;Cross-references: GB:S71484; NID:g240883; PIDN:AAB20650.1; PID:g240884
A;Cross-references: GB:S71484; NID:g240883; PIDN:AAB20650.1; PID:g240884
A;Cross-references: GB:S71484; NID:g240883; PIDN:AAB20650.1; PID:g240884
A;Experimental source: granulocyte
A;Note: sequence extracted from NCBI backbone (NCBIN:71484, NCBIP:71485)
R;Haniu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F.
A;Title: Extracellular domain of granulocyte-colony stimulating factor receptor.
A;Title: Extracellular domain of granulocyte-colony stimulating factor receptor.
A;S68331; MUID:96132662
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R;Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.;

J. Exp. Med. 172, 1559-1570, 1990

A;Title: Expression cloning of a human granulocyte colony-stimulating factor receptor A;Reference number: JH0329; MUID:91079757

A;Accession: JH0330

A;Molecule type: mRNA
A;Residues: 1-680,708-863 <LAR>
A;Residues: 1-680,708-863 <LAR>
A;Note: clone 25-1; placenta
R;Seto, Y.; Fukunaga, R.; Nagata, S.
                                                                                                                                                                  A;Cross-references: GDB:126430; OMIM:138971
A;Map position: lp35-lp34.3
C;Keywords: alternative splicing; glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-863/Product: granulocyte colony-stimulating factor receptor, long form #status p
F;25-680,708-863/Product: granulocyte colony-stimulating factor receptor, short form
F;25-627/Domain: extracellular #status predicted <EXT>
F;658-653/Domain: transmembrane #status predicted <INT>
F;654-863/Domain: intracellular #status predicted <INT>
F;654-863/Domain: intracellular #status predicted <INT>
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J. Immunol. 148, 259-266, 1992
A;Title: Chromosomal gene organization of
A;Reference number: A46486; MUID:92091782
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: GDB:CSF3R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
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A; Residues: 234-269 < HAN
                                 Query Match
Best Local :
4.6%;
larity 20.0%;
Conservative 12
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                                 Score
Pred.
ore 288.5; DB 2;
ed. No. 1.2e-10;
Mismatches 280;
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16486; $68332; $21607
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5, 1990
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                                                                   Length 863;
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granulocyte colony-stimulating factor receptor D7 precursor C; Species: Homo sapiens (man)
C; Date: 12-Feb-1993 *sequence_revision 12-Feb-1993 *text_ch
C; Accession: JH0329; S21608
R; Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.
J. Exp. Med. 172, 1559-1570, 1990
A; Title: Expression cloning of a human granulocyte colony-s
A; Reference number: JH0329; MUID:91079757
A; Accession: JH0329
A; Molecule type: mRNA
A; Residues: 1-783 <LAR>
A; Residues: 1-783 <LAR>
A; Cross-references: GB:X55720; NID:g31698; PIDN:CAA39252.1;
A; Experimental source: placenta
C; Keywords: glycoprotein; transmembrane protein
F; 1-24/Domain: signal sequence *status predicted <SIG>F; 25-783/Pomain: extracellular *status predicted <TRA>
F; 658-653/Domain: transmembrane *status predicted <TRA>
F; 658-783/Domain: intracellular *status predicted <INT>
F; 654-783/Domain: accellular *status predicted <INT>
F; 655-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTLMTLTPEGSELHIILGLFGLLLLLTCLCGTAWLCCSPNRKNPLWPSVPDPAHSSLGSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IFMEGVGKPKIINSFTQDDIEKHQSDAGL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPNPWPQGYVIEWGLGPPSASNSNK----TWRMEQNGRATGFLLKENIRPFQLYEIIVTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSDYKLMYFIIEW-----KNLNEDGEIKW-LRISSSVKKYYIHDHFIPIEKYQFSLYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TFHLPSEAQEVALVAYNSAGTSRPT-PVVFS--ESRGPALTRLHAMARDPHSLWVGW--E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PQAGCLQLCWE-PWQPGLHINQKCELRHKPQRGEASWALVG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INIGLLKISWEKPVFP--ENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPVP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HCCIPRKHLLLYQNMGIWVQAENALGTSMSPQLCLDPMDVVKLEPPMLRTMDPSPEA-AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CQWEPGPETHLPTSFTLKSFKSRG
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    5
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  284;
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Matches 153; Conservative
 674
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VPTIMEEDAFQLPGLGTPPITKLTVLEEDEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDTMKKEKNYTLLWKPLMKNDSLCSVQRYVINHHTS-----CNGTWSEDVGNHTKF 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YELCGLLPATAYTLQIRCIRWPLPGHWSDWS
                                         KGSVCISDQFNSVNFSEAEGTEVTYEDESQRQ
                                                                               LTLMTLTPEGSELHIILGLFGLLLLLTCLCGTAWLCCSPNRKNPLWPSVPDPAHSSLGSW 673
                                                                                                                                                                                                                                               LYQDTMGPSQHVYAYSQEMAPSHAPELHLKHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DLCAV----YAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGP----EFWRIIN 650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETKPRGKFTYDAVYCCNEHECHHRYAELYVID------VNINISCETDGYLTKMT 446
                                                                                                                         CGPLLLEPETISEDISV-
                                                                                                                                                                                                       SHQRMKKLFWEDVPNPKNCSWAQGLNFQ--
                                                                                                                                                                                                                                                                                       IFMEGVGKPKIINSFTQDDIEKHQSDAGL--
                                                                                                                                                                                                                                                                                                                                 PPNPWPQGYVIEWGLGPPSASNSNK----TWI
                                                                                                                                                                                                                                                                                                                                                                                                              TFHLPSEAQEVALVAYNSAGTSRPT-PVVFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFLWTEQAHTVTVLAINSIGASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILS 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PQAGCLQLCWE-PWQPGLHINQKCELRHKPQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INIGLLKISWERPVFP--ENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPVP---- 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HCCIPRKHLLIYQNMGIWVQAENALGTSMSPQLCLDPMDVVKLEPPMLRTMDPSPEA-AP 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVHLGDPITASCIIKQNCSHLDPEPQILWRLG-AELQPGGRQQRLSDGTQESIITLPHLN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTSVGSNVSFHCIYKKE-NKIVPSKEIVWWMNLAEKIPQSQYDVVSD--HVSKVTFFNLN 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -QRQLDPRTVQLFWKPVPLEEDSGRIQGYVVSWRPSGQAGAILPLCNTT-----ELSC 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -FQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP-----SSVKAEIT 548
                                                                                                                                                               -IFW---TNAQNQSFSAILNASSRGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.3%;
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Mismatches 287;
                                                                                                                                                                                                                                               [GKTWAQLEWVPEPPELGKSPLTHYT--- 563
                                                                                                                                                                                                                                                                                                                              RMEQNGRATGELLKENIRPEQLYEIIVTP 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGEASWALVG------PLPLEALQ 291
                                                                                                                                                               VLHGLEPASLYHIHLMAASQAGATNSTV 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P 982
                                                                                                                       SW----KNKDEMMPTTVVSLLSTTDLE 949
                                                                                                                                                                                                                                                                                                                                                                      LRISSSVKKYYIHDHFIPIEKYQFSLYP 813
 P 706
                                                                                                                                                                                                                                                                                                                                                                                                           -ESRGPALTRIHAMARDPHSLWVGW--E 450
                                                                                                                                                                                                                                                                                     -----YVIVPVIISSSILLLGTLLI 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----NCQTQGDSILDCVPKDGQS 184
                                                                                                                                                                                                    ----KPETFEHLFIK-----HTASVT 907
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RESULT 15

JX0312

differentiation-stimulating factor/leukemia inhibitory factor receptor 1 precursor - C; Species: Mus musculus (house mouse)
C; Date: 28-Aug-1985 *sequence_revision 07-Oct-1994 *text_change 01-Dec-2000
C; Accession: JX0312; JC2181; S38942
R; Tomida, M.; Yamamoto-Yamaguchi, Y.; Hozumi, M.
J. Biochem. 115, 557-562, 1994
A; Title: Three different cDNAs encoding mouse D-factor/LIF receptor.
A; Reference number: JX0312; MUID:9434302
A; Accession: JX0312
A; Molecule type: mRNA
A; Residues: 1-1092 <TOM>
A; Cross-references: DDBJ:D26177; NID:g473718; PIDN:BAA05165.1; PID:d1005707; PID:g825
A; Accession: JC2181
A; Molecule type: mRNA
A; Residues: 1-717, 'EA' <TOM1>
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2	VKWDDI 742		68
N	832	8 HDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDD	Оу 798
2 -	TETVIE	VGLGNRIFLTWRHDPNWTCDYVIKWCNSSRSEPCLLDWRKVPSNS	63
7	VXXVVT	T.SAYDINGSCUTUSUTISDSDVKIMVETIEWKUINEDGETKWIDISGS	74
<u>ω</u> ω	KVNIVQS 743 : 1: DITVEQA 631	VGNHTKETELWTEQAHTYTVLAINSIGASVANFNLTESWPMS : : : : : : : : : :	Оу 695 Db 572
₽	571	E-ATPSKGPDTWREWSSDGKNLIVYWKPLPIN	Db 527
4	NGTWSED 694	DIKVPMRGPEFWRIINGDTMKKEKNVTLLWKPLMKNDSLCSVQRYVINHHTSC	Qу 635
4 0	PAYTVVM 634 : EKRHLTT 526	SGKEVQWKMYEVYDAKSKSVSLPVPDLCAVYAVQVRCKRLDGLGYWSNWSNPA::::::::::::::::::::::::::::::::::::	Qy 577 Db 468
7	IEICK		42- (
· · · · ·	4 1	SAVEHRIEGLINETYRLGV-QMHPGQEIHNFTLTG	DD 3/4
7 7		QLRYHRSSLYCSDIPSIHPISEPKDCYLQSDGFYECIFQPIFLLSGYT	4. 6.
ω	ESISGK 373	YGTVVFAGYPPDVPQKLSCETHD-LKEIICSWNPGRITGLVGPRNTEYTLFE	Db 318
2	462	HHRYAEL	Qy 419
7	CNEHEC 418	KEIVWWM-NLAEKIPQSQYDVVSDHVSKVTFFNLNETKPRGKFTYDAVYCC	Oy 364 Db 271
0	: : MSPT 270	: HIDSPHFSGYKE	N
ω	NKIVPS 363	RLDGPGIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCIYKKE	Оу 312
7	VSIRW- 217	PSNATWEIKVLQNPRTEPVALVLLNTMLSGKDTVQHWNWTSDLPLQCATHS	16
<u>.</u>	OVECK .	DIOVOVKYGENGTTUGEADKIVGATGIIVDGIIBOGGVEV	תכ
1 5	PPLVPF 265 : GSALPH 161		Qy 226 рь 105
4	PALSPG 104	KRGVQDLKCTTNNMRVWDCTWPAPLGVSPGTVKDICIKDRFHSCHPL	4
Gi	IFQSP- 225	B KGSFQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQ	Qy 178
57;	92; 71; Gaps	atch 4.5%; Score 281.5; DB 2; Length 109 cal Similarity 18.8%; Pred. No. 4.9e-10; 217; Conservative 177; Mismatches 392; Indels 37	Query Ma Best Loc Matches
; PID:g441494 factor recepto	:d1004778;	n: 538942 preliminary type: mRNA : 1-717,'EA' <tom2> : 1-717,'EA' <tom2> : differentiation; receptor; transmembrane protein ain: signal sequence #status predicted <sig> Product: differentiation-stimulating factor/leukemia in Domain: transmembrane #status predicted <tmm></tmm></sig></tom2></tom2>	A; Accession A; Accession A; Status: A; Molecule A; Residues A; Cross-re C; Keywords F; 1-43/Dom F; 44-1092/F; 828-854/
778; PID:g441494 receptor in mous	ID:d1004	erences: DDBJ:D17444; NID:g441493; PIDN:BAA04258.1; PItal source: liver .; Yamamoto-Yamaguchi, Y.; Hozumi, M. 334, 193-197, 1993 egnancy associated increase in mRNA for soluble D-fact number: S38942; MUID:94039833	;Cross- ;Experi ;Tomida EBS Let ;Title:
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	13 TDSNNEVVSFGSPC 1056	1043	дb
	92 VLLTDKSRVSCPFPAPC 1108	1092	Qy
1042	VVAGYKPOMRLPISPAVEDTAAEDEEGKTAGYRPOANVNTWNLVSPDSPRS	992	д
1091		1035	Qy
991	DVQSMYQPQAKAEEEQDVDPV	971	Дb
1034	76 D-ESQRQPFVKYATLISNSKPSETGEEQGLINSSVTKCFSSKNSPLKDSFSNSSWEIEAQ 1034	976	γQ
970	L1 IVPKIEDTEIISPVAERPGERSEVDPENHVVVSYCPPIIEEEITNPAADEVGGASQVVYI 970	911	망
975	NKDEMMPTTVVSLLSTTDLEKGSVCISDQFNSVNFSEAEG-TEVTYE	930	Qy
910	TFYPDIPNPENCKALQFQKSVCEGSNALKTLEMNPCTPNNVEVLESRS	863	В
929	E	870	QΨ
862)3 HLVLRAYTHGGLGPEKSMFVVTKENSVGLIIAILIPVAVAVIVGVV"SILCYRKREWIKE 862	803	В
869	YVIVPVIISSSILLLGTLLISHQRMKK	843	Ωy
802	PVEELRGFLRGYLFYFQKGERDTPKTRSLEPHHSDIKLKNITDISQKTLRIADLQGKTSY	743	В
842	IEKHQSDAGL	833	δõ

Search completed: May 18, 2002, 06:55:04
Job time: 5694 sec

<u>.</u>"

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Run on:
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May 18, 2002, 06:54:01; Search time 39.61 Seconds (without alignments)
1138.810 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Title: Perfect score: Sequence:

US-08-779-457-2
6254
1 MICQKFCVVLLHWEFIYVIT.....QTCSTQTHKIMENKMCDLTV 1165

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

333222222222222 33322222222222222 33222222	Result No.
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P VARIANTS ARG-109; ARG-223 AND ASN-656.

REDLINE=97318795; PubMed=9175732;

A Gotoda T., Manning B.S., Goldstone A.P., Imrie H., Evans A.L.,

Strosberg A.D., McKeigue P.M., Scott J., Aitman T.J.;

A Strosberg A.D., McKeigue P.M., Scott J., Aitman T.J.;

PLEPTIN receptor gene variation and obesity: lack of association white British male population.";

Hum. Mol. Genet. 6:869-876(1997).

-i- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).

-i- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).

-i- SUBCELLULAR LOCATION: Type I membrane protein.

-i- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.

-i- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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EMBL; U59263; AAB09673.1.
EMBL; U59249; AAB09673.1.
EMBL; U59250; AAB09673.1.
EMBL; U59252; AAB09673.1.
EMBL; U59252; AAB09673.1.
EMBL; U59254; AAB09673.1.
EMBL; U59255; AAB09673.1.
EMBL; U59256; AAB09673.1.
EMBL; U59258; AAB09673.1.
EMBL; U59259; AAB09673.1.
EMBL; U59259; AAB09673.1.
EMBL; U59250; AAB09673.1.
EMBL; U59250; AAB09673.1.
EMBL; U59261; AAB09673.1.
INTERPOOP : IPRO02996; CR1/
INTERPOO; IPRO03961; FN_INTERPOO; IPRO03961; FN_INTERPOO; IPRO03961; FN_INTERPOO; IPRO03961; FN_INTERPOO; IPRO03529; Hemmore interpoo; IPRO03529; Hemmore interpoor; IPRO03529; Hemmore interpoor i
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Siegfried W., Maye
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                                                           SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VASTRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY; TISSUMEDLINE-96295531; PubMed-8702432; Iida M., Murakami T., Ishida K., Mizuno A., Ku "Substitution at codon 269 (glutamine --> prol receptor (OB-R) cDNA is the only mutation four (fa/fa) rat."; Biochem. Biophys. Res. Commun. 224:597-604(1956)
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Q62959; Q63007; P70493; P70494; P70499
P97589; O35772;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
Leptin receptor precursor (LEP-R) (OB
LEPR OR OBR OR FA.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata
Mammalia; Eutheria; Rodentia; Sciurogo
NCBI_TaxID+10116;
[1]
SEQUENCE FROM N.A., AND VARIANT FA PROSTRAIN-ZUCKER; TISSUE-Hypothalamus;
MEDLINE-96241565; PubMed-8673096;
Phillips M.S., Liu Q., Hammond H.A., J
Hess J.F.;
  SEQUENCE FROM N.A., AND VARIANT FOR STRAIN-SPRAGUE-DAWLEY, AND ZUCKER MEDLINE-96332408; PubMed-8769097;
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"Leptin receptor missense municipal municipal
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RP VARIANT FA PRO-269.

RX MEDLINE-96314329; PubMed-8690163;
RA Chua S.C. Jr., White D.W., Wu-Peng X.S., Liu S.M. Okada N.,
RA Chua S.C. Jr., White D.W., Wu-Peng X.S., Liu S.M. Okada N.,
RA Kershaw E.E., Chung W.K., Power-Kehoe L., Chua M., Tartaglia L.A.,
RA Leibel R.L.;
RT "Phenotype of fatty due to Gln269pro mutation in the leptin receptor
RT (Lept).";
RL Diabetes 45:1141-1143(1996).
C-1- FUNCTION: RECEPTOR FOR MESITY FACTOR (LEPTIN).
C-1- FUNCTION: THE SHORT FORM (VARIANT A) MAY ACT TO TRANSPORT LEPTIN
CC-1- FUNCTION AS A TRANSPORT PROTEIN.
CC-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXCEPT FOR FORM E
WHICH COULD BE SECRETED.
C-1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; A. B (SHOWN HERE), C, D AND E;
ARE PRODUCED BY ALTERNATIVE SPLICING.
C-1- SUSSEASE: THE FATTY (FA) MUTATION PRODUCES PROFOUND OBESITY OF
EARLY ONSET CAUSED BY HYPER-HAGIA, DEFECTIVE MONSHIVERING
THERMOGENESIS, AND PREFERENTIAL DEPOSITION OF ENERGY INTO ADIPOSE
TISSUE.
-1- SIMILARITY: BELONGS TO THE
-1- SIMILARITY: BELONGS TO THE
 SEQUENCE FROM N.A., AND VARIANT FA PRO-21 STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY; MEDLINE-96212906; PubMed-8630068; Iida M., Murakami T., Ishida K., Mizuno 1 "Phenotype-linked amino acid alteration: zucker fatty (fa/fa) rat."; Biochem. Biophys. Res. Commun. 222:19-26(6)
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SEQUENCE OF 843-892 FROSTRAIN-SPRAGUE-DAWLEY;
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n in leptin receptor cDNA from
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TISSUE-Choroid plexus;

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STRAIN=BALB/C; TISSUE=Liver;
MEDLINE=96206286; PubMed=8616721;
Cioffi J.A., Shafer A.W., Zupancic T
Mikhail A., Platika D., Snodgrass H.]
"Novel B219/OB receptor isoforms: po:
hematopoiesis and reproduction.";
Nat. Med. 2:585-589(1996).
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MEDLINE-97462708;
Igel M., Becker W.
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SEQUENCE
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STRAIN-C57BL/KSJ; TISSUE-Hypothalamus
MEDLINE-96190816; PubMed-8608603;
Chen H., Charlat O., Tartaglia L.A., V
Ellis S.J., Lakey N.D. Colocomo.
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suppression is required to transcripts.";
Genomics 45:264-270(1997).
                                                                                                                                                                                                                                                Proc.
[7]
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"Hyperleptinemia, leptin resistance,
in the New Zealand obese mouse.";
Endocrinology 138:4234-4239(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ellis S.J., Lakey N.D., Culpepper J., Moore R
Duyk G.M., Tepper R.I., Morgenstern J.P.;
"Evidence that the diabetes gene encodes the
identification of a mutation in the leptin re
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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Lee J.I., Friedman J.M.;
"Abnormal splicing of the
Nature 379:632-635(1996).
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-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXCEPT FOR FORM E WHICH COULD BE SECRETED.

-!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; A, B (SHOWN HERE), C, D AND E; ARE PRODUCED BY ALTERNATIVE SPLICING.

-!- TISSUE SPECIFICITY: (1) VARIANT A: HIGHEST LEVEL OF EXPRESSION IN LUNG AND KIDNEY, ALSO PRESENT IN CHOROID PLEXUS AND HYPOTHALAMUS.

(2) VARIANT B: HIGHEST LEVEL OF EXPRESSION IN HYPOTHALAMUS AND LOWER LEVEL IN BRAIN, TESTES AND ADIPOSE TISSUE. (3) VARIANT E: EXPRESSED IN ADIPOSE TISSUE, HYPOTHALAMUS, HEART, AND TESTES.

-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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A -> T (IN REF. 5).
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   RP SEQUENCE FROM N.A.

RC STRAIN=ICR; TISSUE-Macrophage;

RX MEDLINE-9291532; PubMed=1602143;

RA MEDLINE-9291532; PubMed=160214;

RA MEDLINE-9291532; PubMed=160214;

RESULTING OF AN MILT-11 CAN UTILIZE GP130 FOR INITIATING COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES, AND TRANSDUCES THE SIGNAL DOES NOT BIND IL-6. MAY HAVE A ROLE IN EMBRYONIC DEVELOPMENT.

C -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

C -!- SUBCELLULAR LOCATION: Type I membrane protein.

SPLEEN, KIDNEY, LUNG AND LIVER, FOUND IN ALL THE CELL LINES TESTED EXCEPT BAF-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE
                                                                                                                                                                                                                                     Eukaryota; Metazoa; (Mammalia; Eutheria; NCBI_TaxID=10090; [1]
                                                                                                                                                                                                                                                                                 IL6B_MOUSE STANDARD; PRT; 917 AA.

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Q00560;
01-FEB-1995 (Rel. 31, Created).
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin 6 signal transducer) (Membrane glycoprotein 130) (GP130).

IL6ST.

Mus musculus (Mouse).
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                                                                                                                                                                                                                                                              Chordata;
Rodentia;
I ALPHA AND A PARTY I MEMBRANE PROTEIN.

IN TISSUES SUCH AS BRAIN, HEART, THYMUS,
INTER, FOUND IN ALL THE CELL LINES TESTED
INTER TARRESTED TO IL-6-RESPONSIVE
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EMBL; M83336; AAA37723.1; -.

HSSP; P40189; 1BQU.

MGD; MGI:96560; I16st.

InterPro; IPR002996; CR1A.

InterPro; IPR003961; FN_III.

InterPro; IPR003952; FnIII_repeat.

InterPro; IPR003529; Hematopo_receptor_L_F2.

Pfam; PF00041; fn3; 4.

PRINTS; PR00014; FNTYPEIII.

SMART; SM00060; FN3; 2.

PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
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European Bioinformatics Institute. Tr
European Bioinformatics Institutions as long
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SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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QNVYGVTMLSGFPPDKPTNLTCIVNEG
                                            AELYVI - -
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
SER-RICH.
BY SIMILARITY.
BY SIMIL
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Pred. No. 5.9e-17;
); Mismatches 338;
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INTERLEUKIN-6
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C P40189; Q9UQ41;

C P40189; Q9UQ41;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin Merican deceptor) (Membrane glycoprotein 130) (GP130) (Oncostatin Merican deceptor) (CDw130) (CD130 antigen).

The receptor (CDw130) (CD130 antigen).
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PubMed=2261637;
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[4]
X-RAY CRYSTALLOGRAPHY (
YFDLINE-98169383; PubMonton D.,
                                                                InterPro; IPR002996; CRIA.
InterPro; IPR003961; FN_III.
InterPro; IPR003962; FnIII_repeat.
InterPro; IPR0039529; Hematopo_receptor_L_
InterPro; IPR003529; Hematopo_receptor_L_
Pfam; PF00041; fn3; 3.
PRINTS; PR00014; FNTYPEIII.
SMART; SM00060; FN3; 3.
PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
Receptor; Transmembrane; Glycoprotein; Im
Repeat; 3D-structure; Alternative splicin
                                                                                                                                                                                                                                                                                                                                               EMBL; M57230;
EMBL; AB015706
PIR; A36337; A
PDB; 1BQU; 26-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.

X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.

MEDLINE-98169383; PubMed-9501088;

Bravo J., Staunton D., Heath J.K., Jones E.Y.;

"Crystal structure of a cytokine-binding region of gp130.";

EMBO J. 17:1665-1674(1998).

-I- FUNCTION: Signal-transducing molecule. The receptor systems for IL-6, LIF, OSM, CNTF, IL-11 AND CT-1 can utilize gp130 for initiating signal transmission. Binds to IL-6/IL-6-R (alpha chain) complex, resulting in the formation of high-affinity IL-6 binding sites, and transduces the signal Does not bind IL-6. May have a role in embryonic development (By similarity).

-!- SUBUNIT: Heterodimer of an alpha and a beta chain.

-!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1) and secreted (isoform 2).

-!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/gp130-RAPS; are produced by alternative splicing.

-!- TISSUE SPECIFICITY: Found in all the tissues and cell lines examined. Expression not restricted to IL-6 responsive cells.

-!- DISEASE: gp130-RAPS is an autoantigen found in rheumatoid arthritis (RA) but it is not specific to patients with RA.

-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

-!- DATABASE: NAME-PROW; NOTE-CD guide CD130 entry;

WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd130.htm".
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"Crystal s
EMBO J. 17
                                                 Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Murakami M., Nakao K.;
"Cloning of novel soluble gp130 and detection
autoantibodies in rheumatoid arthritis.";
T Clin. Invest. 106:137-144(2000).
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MEDLINE-20341529; PubMed-10880057;
Tanaka M., Kishimura M., Ozaki S.,
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Cell 63:1149-1157(1990)
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"Molecular cloning
gp130.";
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BL; AB015706; BAA78112.1;
R; A36337; A36337.
3; 1BQU; 26-AUG-98.
4; 600694; -.
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Nakao K.;
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IL-6 signal
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and N-glycosylation
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CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
SER-RICH.
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Wang Y., Nesbitt J.E., Fuentes N.L., Ful
"Molecular cloning and characterization
transducing molecule, gp130.";
Genomics 14:666-672(1992).
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Repeat.
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P40190;

01-FEB-1995 (Rel. 31, Created)

01-FEB-1995 (Rel. 31, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Interleukin-6 receptor beta chain precursor (IL-6R-beta)

6 signal transducer) (Membrane glycoprotein 130) (GP130)
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
[1]
                                                                                                                                     EMBL; M92340; -; NOT_ANNOTATED_CDS
PIR; A44257; A44257.
HSSP; P40189; 1BQU.
                                                                                                                                                                                                                                                                                           IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES, AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN EMBRYONIC DEVELOPMENT (BY SIMILARITY).

-!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS AND ENDOTHELIAL CELLS.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 signal transducer) IL6ST.
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                                          Receptor;
                                                       PROSITE;
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                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                                                                                 rPro; IPR002996; rPro; IPR003961; rPro; IPR003529; pF00041; fn3; 3
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un email to license@isb-sib.ch).
                                          Transmembrane;
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FN_III.
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                                       O_REC_L_F2; 1 Glycoprotein;
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Sciurognathi; Muridae
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Murinae; Rat
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                    NKYILEWCVLSENSPCIPDWQQEDGTVNRTHLRGSLLESKCYLITVTPVFPGGPGSPESM 509
                                        MYFIIEWKNLNEDGEI
                                                                                AHTVTVLAINSIGASVANFNLTFSWPMSKV-NI
                                                                                                      ANHPQEYRSARLIWKTLPLSEANGKILDYEVVLTQSKSVSQTYTV---NGTELIVNLTNN 393
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                                                                                                                                                                                       PPHNLSVTNSEELSSILKLAWVNSGLDSILRLKSDIQYRTKDAST -----WIQVPLEDTV 277
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                                                             RYVASLAARNVVGKSPATV-LTIPGSHFKASHPVVDLKAFP-KDNLLWVEW--TPPSKPV 449
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FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
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CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
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Mismatches 326;
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KAYLKQAAPSKGPTVRTKKVGKNEAVLEWDHLPVDVQNGFIRNYSISYRTSVGKEMVVRV 569

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AC P40223;
DT 01-FEB-1995 (
DT 01-FEB-1995 (
DT 30-MAY-2000 (
DE Granulocyte c
GN CSF3R OR CSFG
OS MUS MUSCUlus
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OC Mammalia; Eut
OX NCBI_TaxID=1(
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RA FUKUNAGA R.,
RT "EXPRESSION (
RT Stimulating; Eut
OX MEDLINE=9023;
RA FUKUNAGA R.,
RT "SCHUCTURE BY
RX MEDLINE=9733;
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01-FEB-1995 (Rel. 31, I
30-MAY-2000 (Rel. 39, I
Granulocyte colony stin
CSF3R OR CSFGR.
                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    motif of the granulocyte colony-stimulating factor receptor and in interaction with ligand.";
Nat. Struct. Biol. 4:498-504(1997).

-!- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR.
ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION EVENTHE CELL SURFACE.

-!- SUBUNIT: DIMER (PROBABLE).

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- TISSUE SPECIFICITY: FOUND IN BONE MARROW.

-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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MEDLINE-90235283; PubMed-2158861;
Fukunaga R., Ishizaka-Ikeda E., Seto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Memmalia; Eutheria; NCBI_TaxID=10090;
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MEDLINE-97331327; PubMed-9187659;
Yamasaki K., Naito S., Anaguchi H., Ohkubo T.,
"Solution structure of an extracellular domain
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     L; M58288; AAA37673.1;
; A34898; A34898.
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; 1CTO; 22-OCT-97.
; MGI:1339755; Csf3r.
erPro; IPR002996; CR1A.
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ECTIN TYPE-III 2.
ECTIN TYPE-III 3.
ECTIN TYPE-III 4.
ECTIN TYPE-III 5.
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                                                                                                                                                                                                                                              ANWTL--VFHLPSSKDQF---ELCGLHQA 301
                                                                                                                                                                                                                                                                             VQWKMYEVYDAKSKSVSLPVPDLCA---- 605
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                                                                  VQSLSAYPLNSSCVIVSW---ILSPSDY 765
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MEDLINE-92007727; PubMed-1915266;

Gearing D.P., Thut C.J., Vandenbos T., Gimpel King J., Price V., Cosman D., Beckmann M.P.;

"Leukemia inhibitory factor receptor is struct IL-6 signal transducer, gp130.";

EMBO J. 10:2839-2848(1991).
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01-NOV-1995
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use by non-profit institute. The modified and this statement is not removed. entities requires a license agreement.
                                                                        This
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                                                                                       WITH GP130. THE SOLUBLE FORM INHIBITS THE BIOLOGICAL ACTIVITY LIF BY BLOCKING ITS BINDING TO RECEPTORS ON TARGET CELLS.

-!- SUBUNIT: HETERODIMER COMPOSED OF LIFR AND GP130.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THERE IS A MEMBRANE-BOUND AND A SECRETED FORM.

-!- ALTERNATIVE PRODUCTS: THE SECRETED AND THE MEMBRANE-BOUND FORMY ARISE BY ALTERNATIVE SPLICING.

-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                             SWISS-PROT entry is copyright. It een the Swiss Institute of Bioinf European Bioinformatics Institute.
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Q99062;
01-FEB-1995 (Rel. 31, C
01-FEB-1995 (Rel. 31, L
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Granulocyte colony stim
(CD114 antigen).
CSF3R OR GCSFR.
                      MEDLINE-Placenta;
MEDLINE-91079757; PubMed-2147944;
Larsen A., Davis T., Curtis B.M., Gimpel S., Sims J.E., Cosmar Park L., Sorensen E., March C.J., Smith C.A.;
"Expression cloning of a human granulocyte colony-stimulating receptor: a structural mosaic of hematopoietin receptor, immunoglobulin, and fibronectin domains.";
J. Exp. Med. 172:1559-1570(1990).
                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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EMBL; EMBL; EMBL; PIR;

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CAA39253.1; CAA39252.1; AAB20660.1; AAA63176.1; AAA63177.1; AAA63178.1; JH0329.

EMBL; EMBL;

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Fukunaga R., Isniauna
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STRUCTURE BY NMR OF 227-334.
STRUCTURE BY NMR OF 227-334.
MEDLINE-97331327; PubMed-9187659;
Yamasaki K., Naito S., Anaguchi H.,
Yamasaki K., Naito S., Anaguchi H.,
                                                                                                  the
                                                                                                                                                                             GCSFR-2, GCSFR-3 AND GCSFR-4/D7; SEEM TO BE PRODUCED BY
ALTERNATIVE SPLICING.

-!- TISSUE SPECIFICITY: ONE OR SEVERAL FORMS HAVE BLEN FOUND IN
MYELOGENOUS LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL LINE,
BONE MARROW CELLS, PLACENTA, AND PERIPHERAL BLOOD GRANULOCYTES
THE GCSFR-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. TH
GSCFR-3 FORM IS HIGHLY EXPRESSED IN PLACENTA.

-!- DISEASE: DEFECTS IN CSF3R ARE A CAUSE OF KOSTHANN SYNDROME;
ALSO KNOWN AS SEVERE CONGENITAL NEUTROPENIA (SCN).

-!- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.

-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

-!- DATABASE: NAME-PROW; NOTE=CD guide CD114 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd114.htm".
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Nat. Struct. Biol. 4:498-503(1997).
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J. Immunol. 148:259-266(1992).
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                                                                    s SWISS-PROT entry is copyright. I ween the Swiss Institute of Bioin European Bioinformatics Institute by non-profit institutions as
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Ishizaka-Ikeda E., Pan
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Y., Mizushima S.,
nRNAs encoding huma
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                     It is produced through a collaboration formatics and the EMBL outstation formatics are no restrictions on its long as its content is in no way emoved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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                                                                        Tomida M.,
"Pregnancy receptor in
FEBS Lett.
[3]
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SEQUENCE FROM N.A. (SECKELL. SEQUENCE FROM N.A. (SECKELL. STRAIN-ICR; TISSUE-Liver;
MEDLINE-94039833; PubMed-7901054;
MEDLINE-94039833; PubMed-7901054;
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MEDLINE-94039833; PubMed-7901054;
MEDLINE-94039833; PubMed-7901054;
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MEDLINE=92007727; PubMed=1915266;
Gearing D.P., Thut C.J., Vandenbos T.,
King J., Price V., Cosman D., Beckmann
"Leukemia inhibitory factor receptor 1:
IL-6 signal transducer, gpl30.";
EMBO J. 10:2839-2848(1991).
   SEQUENCE FROM N.A MEDLINE=94334302; Tomida M., Yamamo
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                    y associated increase in mouse liver.";
334:193-197(1993).
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n M.P.;
is structurally related to the
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mi M.,
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EMBL; D17444; BAA04258.1; -.
MGD; MGI:96788; L1fr.
InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor_L_F2.
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J. Blochem. 115:557-562(1994).
-!- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. MAY HAVE A COMMON WITH GP130. THE SOLUBLE FORM INHIBITS THE BIOLOGICAL ACTILIF BY BLOCKING ITS BINDING TO RECEPTORS ON TARGET CELLS.
-!- SUBUNIT: HETERODIMER COMPOSED OF LIFR AND GP130.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THERE IS A MEMBRANE-BOUND AND A SECRETED FORM.
-!- ALTERNATIVE PRODUCTS: THE SECRETED AND THE MEMBRANE-BOUND MAY ARISE BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: PLACENTA, LIVER, KIDNEY, HEART, LUNG,
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THE SECRETED FORM.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; PF00041; f
T; SM00060;
                                                     KGSFQMVHCNCSVHECCECLVPVP-----TAK---LNDTLLMC--LKITSGGVIFQSP-
                  KRGVQDLKCTTNNMRVWDCTWPAPLGVSPGTVKDICIKDRFHSCHPLETTNVKIPALSPG
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Transmembrane; Glycoprotein; Immunoglobulin
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CYTOPLASMIC
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                                                                                281.5; up .,
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. ~+~hes 392;
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                                                                     AFFILSDQHPNI---
                                                                                                           DVQSMYQPQAK-
                                                                                                                                                                                IVPKIEDTEIISPVAERPGERSEVDPENHVVVSYCPPIIEEEITNPAADEVGGASQVVYI 970
                                                                                                                                                                                                                 NKDEMMPTTVVSLLSTTDLEKGSV
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                                                                                                                                                                                                                                                                                       LFWEDVPNPKNCSWAQGLNFQKPETFEHLFIKHTASVTCGPLLLEPETISEDISVDTSWK 929
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                                                                                                                                         -ESOROPFVKYATLISNSKPSETGEEQGLINSSVTKCFSSKNSPLKDSFSNSSWEIEAO
                                     -VVAGYKPQMRLPISPAVEDTAAEDEEGKTAGYRPQANVNTWNL----VSPDSPRS-- 1042
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                                                           ISPHLTFSEGLDELLKI
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                                                                 EGNFPEENNDKKSIYYLGVTSIKKRESG 1091
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Mammalia; Euthería; P
NCBI_TaxID=9606;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Interleukin-12 receptor beta-2 chain precurso
2) (IL-12R-beta2).
IL12RB2.
CARBOHYD
SEQUENCE
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Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabav Gately M.K., Gubler U.;
"A functional interleukin 12 receptor complex is combeta-type cytokine receptor subunits.";
Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).
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                                                                                                                                                                                                                                                                                                                                                                      InterPro;
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                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                    SMART;
                                                                                                                                                                                                                                                                                                                                                    Pfam;
                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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SUBUNIT: DIMER/OLIGOMER;
AFFINITY IL-12 RECEPTOR |
IL12RB2.
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                                                                                                                                                                                                                                                                                                                                                 PF00041;
                                                                                                                                                                                                                                                                                                                 SM00060; F
E; PS01353;
                                                                                                                                                   Transmembrane;
1 21
2 862
22 862
22 624
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IPR003961;
IPR003529;
 AAB36675.1;
1BQU.
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BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS
CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
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nbrane; Glycoprotein; Signal;
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Primates;
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FN_III.
Hematopo_receptor_L
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CYTOPLASMIC (POTENTIAL FIBRONECTIN TYPE-III 1 FIBRONECTIN TYPE-III 2 FIBRONECTIN TYPE-III 3 N-LINKED (GLCNAC. ...)
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Catarrhini; Hominidae;
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                                                                                                                                                                     AGDLPT----HDGYLPSNIDD-LPSHEAPLADSLE----ELEPQHISLSVFPSSSLHP-- 839
                                                                                                                                                                                                   SNSKPSETGEEQGLINSSVTKCFSSKNSPLKDSFSNSSWEIEAQ----AFFILSDQHPNI 1046
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182; Conser
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                               STANDARD;
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tches 322;
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InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hematopo
Pfam; PF00041; fn3; 4.
SMART; SM00060; FN3; 4.
PROSITE; PS01352; HEMATOPO_RE
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MEDLINE=94283267; PubMe
Chen X., Horseman N.D.
"Cloning, expression, a
receptor.";
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Prolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Use entitles requires a license agreement (See http. or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Columba livia (Domestic pigeon)
Eukaryota; Metazoa; Chordata; C
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced the between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no use by non-profit institutions as long as its cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endocrinology 135:269-276(1994).
-I- FUNCTION: THIS IS A RECEPTOR PROLACTIN.
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HSSP; P16471; 1BP3.
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Local Similarity 20.8%;
nes 165; Conservative 1
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SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF REC
SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE
                   GSLDSPPTCVLPDSVVKPLPP--SSVKAEITINIGLLKISWEKPVFPE
 GSNSSDPQYVDVT
                                                             IPSIHPISEPKDCYLQSDGFYECIFQPIFLLSG
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nbrane; Glycoprotein;
23 POTENTIAL.
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precursor (PRL-R).
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CYTOPLASMIC
FIBRONECTIN
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; Columbiformes; Columbidae; Columba.
SIMILARITY.
SIMILARITY.
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No. 3.9e-07;
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P97378;

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Interleukin-12 rece

2) (IL-12R-beta2).

IL12RB2.
                                                                                                                                                                                                                               Mus musculus (Mouse)
Eukaryota; Metazoa; Mammalia; Eutheria;
NCBI_TaxID=10090;
        beta-type cytokine receptor Proc. Natl. Acad. Sci. U.S.: -!- FUNCTION: INVOLVED IN II
                                                                              SEQUENCE FROM N.A.
MEDLINE=97098510; PubMed=894:
Presky D.H., Yang H., Minetti
Gately M.K., Gubler U.;
"A functional interleukin 12
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H., Minetti L.J
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Rodentia;
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Last sequences
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A. 93:1400
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Sciurogo
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                                                                                                                                Chua A.O., Nabavi N., Wu C.-Y.,
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12-14007(1996).
DUCTION. BINDS TO IL-12 WITH A
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[nath1; Muridae; Murinae; Mus.
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                                                                              complex is composed of two
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SUBCELLULAR LOCATION: Type I membrane protein.
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                                                  Type I membrane protein
THE CYTOKINE FAMILY OF RECEPTORS.
FIBRONECTIN TYPE III-LIKE DOMAINS.
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                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasianinae;
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(CPRLP).
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THE ANTERIOR PITUITARY HORMONE
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There are no
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is produced through a collaboration rmatics and the EMBL outstation . There are no restrictions on its
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Best Local Similarity 20.4%; P
Matches 174; Conservative 127;
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EMBL; D13154; BAA02439.1; -.

PIR; JQ1655; JQ1655.

HSSP; P14787; 1AN3.

InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003961; FN_III.

SMART; SM00060; FN3; 4.

SMART; SM00060; FN3; 3.

PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
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PNDERVKDMIVWIVLGVLSSLICLIMSWTMVLKGYRMITFMLPPVPGPK--
                                                                                                     DGEIKWLRISSSYKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKH---
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                                                                                 EGE-EWETIFVGQQTQYKMFSLNPGKKYIIQIH-
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                                         -QSDAGLYVIVPVIISSSILLLG-TLLISHQRMKKLFWEDVPNPKNCSWAQGLNFQ
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Glycoprotein;
POTENTIAL.
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENLINKED (GLCNAC
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Pred. No. 2e-0
?7; Mismatches
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NO. 2e-06;
---hes 291;
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Qy	891 KPETTASVT- 907	
Db	487 LLETGKSEELLSALGCHGLPPTSDCEELLIEYLEVEDSEDQQLMPSHDNGHPSKNAKITR 546	
Qy	NKDEMMP	
В	547 KETDSDSGRGSCDSPSLLSEKCRETCALPPVLQTQEVRDVQEKKAAKRSWETQYVASE 604	
Qy	SLLSTTDLEKGSVCISDQF-NSVNFSEAEGTEVTYEDES	
₽b	: :: : : 605 RKALLSNSESAKSSTWPAVQLPNSQPPMFAYHSIVDAHKITLNTTNTNVAAVLVEDEEEH 664	
Qy	TGEEQGL	
Db	665 QSQCSLTETIPGEMEKQ-GEMENLHSKTEQTTAQVKQNRSNERLPFLDAALMDYVEVHK- 722	
Qy	1035 AFFILSDQHPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIYYLGVTSIK 1086	
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Qy	- ∺	
ఠ	763 DHNILVLMPD-SRVP-HTPASQEPAKETSQSLQQGQVEKNXSYCLTAPSDCKRETG 816	
Qy :	SYMPQE	
Дb	817 GSEYMDPSSFMPSFK 831	
Fü	LT 15 _MELGA PRLR_MELGA STA	
a d d	(91091; (91092; 1997 (Rel. 35, Created) 1997 (Rel. 35, Last sequence upda	
	L-1999 (Rel. 38, Last annotation ctin receptor precursor (PRL-R)	
	ris gallopavo (Common turkey). ota; Metazoa; Chordata; Craniata; Vertebrata	
	osauria; Aves; Neognathae; Galliformes; Meleagrididae; _TaxID=9103;	
	SEQUENCE FROM N.A.	
. . .	LINE-97057891; PubMed-8902221;	
	ar cloning, tissue distribution, and expression of the	
	n receptor during various reproductive states in o.";	
	Biol. Reprod. 55:1081-1090(1996).	
	ž	
	ts G.R., You S.K., Foster D.N., el Halawani M.E.;	
	995) to the EMBL/GenBank/DDB	
	PROLACTIN. 1- SUBCELLULAR LOCATION: Type I membrane protein.	
	- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.	
	SWISS-PROT entry is copyright. It is produced through a collaborat	101
	Swiss Institute of Bioinformatics and the EMBL outstation	<u> </u>
	by non-profit institutions as long as its content is in no	Walt
	dified and this statement is not removed. Usage by and for commerc titles requires a license agreement (See http://www.isb-sib.ch/announ	ía. Ce,
	r send an email to	
	EMBL; L76587; AAB01544.1; EMBL; U22947; AAA75038.1;	

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SMART; SM00060; F
PROSITE; PS01352;
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InterPro; IPR003961;
InterPro; IPR003528;
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P16471;
                                                                 MKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINS
                                                                                                      VRSGWLTLDYELRLKPEEGEEWETVF--VGQQTQYKMFSLNPGKK--
                                                                                                                                                                                            PKILTSVGSNVSFHCIYKKENKIV--
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 NLTFSWPMSKVNIVQSLS--AYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNEDGEIKW
                                   VLSSLICLIM-
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1BP3.
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mbrane; Glycoprotein;
23 POTENTIAL
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FN_III.
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                                    SWIMVLKGYRMITFILPPVP
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Pred. NO. 4.2e-(
26; Mismatches 2
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TYPE-III 1.
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TYPE-III 4.
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Search completed: May 18, 2002, 07:02:46 Job time: 525 sec

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ALIGNMENTS

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RESULT
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                                                                                                                  "A role for leptin and its cognate receptor in hematopoiesis.";

Curr. Biol. 6:1170-1180(1996).

R EMBL; U66497; AAB07497.1; -.

R HSSP; P16471; 1BP3.

R InterPro; IPR002996; CR1A.

R InterPro; IPR003961; FN_III.

R InterPro; IPR003529; Hematopo_receptor_L_F2.

R InterPro; IPR003531; Hematopo_receptor_S_F1.

R Ffam; PF00041; fn3; 2.

R Pfam; PF00041; fn3; 2.

R MART; SM00060; FN3; 1.

R PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.

R PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.

W Receptor.

O SEQUENCE 1165 AA; 132493 MW; CAA03BEAF2602D0A CKC64;
                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1165; Conservative
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Q1-FEB-1997 (TrEMBLrel. 0
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LEPTIN RECEPTOR.
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=96398968; PubMed=8805376;

Bennett B.D., Solar G.P., Yuan J.Q.,
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Mammalia; Eutheria;
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MICQKECVVLLHWEETYVITAENLSYPITPWREKLSCMPPNSTYDYELLPAGLSKNTSNS 60
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Macaca mulatta (Rhesus macaque).
QC Eukaryota; Metazoa; Chordata; Craniata; OC Mammalia; Eutheria; Primates; Catarrhin QC Cercopithecinae; Macaca.
NCBL_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98408931; PubMed=9738551;
RX MEDLINE
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Best Local Similarity 95.6%;
Matches 1114; Conservative
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FN_III.
Hematopo_receptor_L_F2.
Hematopo_receptor_S_F1.
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o. 0;
                     DVIYFPPKILTSVGSNVSFHCIYKKENKI 360
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Bank/DDBJ databases.
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i; Cercopithecidae;
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RESULT 3
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ID Q9MYL0;
AC Q9MYL0;
DT 01-OCT-2000 (TrEMBLrel. 15, Creat
DT 01-DEC-2001 (TrEMBLrel. 19, Last
DT 01-DEC-2001 (TrEMBLrel. 19, Last
DE LEPTIN RECEPTOR LONG INSERT ISOFO
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Cra
OC Mammalia; Eutheria; Primates; Cat
OC Mammalia; Eutheria; Macaca.
OX NCBI_TaxID-9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ADIPOSE TISSUE;
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TLLWKPLMKNESLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
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Last sequence update)
Last annotation updat
ISOFORM.
                                      Craniata;
Catarrhini
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                                      Vertebrata; Euteleostomi;
.; Cercopithecidae;
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Matches 1114; Conservative
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Hotta K., Gustafson T.A., Ortmeyer H.K.,
"Monkey leptin receptor mRNA: sequence, t
expression in the adipose tissue of norma
2 diabetic rhesus monkeys.";
Obes. Res. 6:353-360(1998).
[2]
SEQUENCE FROM N.A.
TISSUE-ADIPOSE TISSUE;
Hotta K., Gustafson T.A., Ortmeyer H.K.,
Submitted (JAN-2000) to the EMBL/GenBank,
EMBL; AF225874; AAF35388.1; -
HSSP; P16471; 1BP3.
InterPro; IPR003961; FN_III.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor_L_
InterPro; IPR003531; Hematopo_receptor_S-
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1
PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKN-
PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKN-
Receptor.
SEQUENCE 1194 AA; 135824 MW; 76D023E6
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18; Mismat
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normal, hyperinsulinemic, and type
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                      MDIKVPMRGPEFWRIINGDTMKKEKNV 660
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Submitted (SEP-1998) to the EMBL/GenBank/DDBJ (2)

SEQUENCE OF 408-470 FROM N.A.

MEDLINE-97222487; PubMed-9069130;

Ernst C.W., Kapke P.A., Yerle M., Rothschild M.

"The leptin receptor gene (LEPR) maps to porcin

Mamm. Genome 8:226-226(1997).

EMBL; AF092422; AAC61766.1; -.

EMBL; U72070; AAC48707.1; -.

HSSP; P16471; 1BP3.

InterPro; IPR00396; CR1A.

InterPro; IPR003951; FN_III.

InterPro; IPR003529; Hematopo_receptor_L_F2.

InterPro; IPR003531; Hematopo_receptor_S_F1.

Pram; PF00041; fn3; 1.

SMART; SM00060; FN3; 2.

PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa (Pig).
Eukaryota; Metazoa; (
Mammalia; Eutheria; (
NCBI_TaxID=9823;
[1]
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01-JUL-1997 (
01-MAY-1999 (
01-JUN-2001 (
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Murphy B.D.;
"Porcine leptin (
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InterPro; IPR003531; Hematopo_receptor_S_F1.
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1
PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1
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Mammalia; Eutheria; E
NCBI_TaxID=9606;
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SEQUENCE FROM N.A.
MEDLINE=96398968; Pub
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LEPTIN RECEPTOR.
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"A role for leptin and its cognate Curr. Biol. 6:1170-1180(1996).
EMBL; U66496; AAB07496.1; -.
HSSP; P16471; 1BP3.
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Thervota; Metazoa; Chordata;
Theria; Primates;
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MEDLINE-97215244; PubMed-9061609;

Luoh S.M., Di Marco F., Levin N., Armanin:

Bennett G.L., Williams M., Spencer S.A.,

Cloning and characterization of a human

r biologically active leptin immunoadhesin.

L J. Mol. Endocrinol. 18:77-85(1997).

R EMBL; U66495; AAB07495.1; -.
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                                     Armanini M., Xie M.H., Nelson C., r S.A., Gurney A., de Sauvage F.J.; human leptin receptor using a adhesin.";
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Best Local Similarity 100.0%;
Matches 891; Conservative (
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HSSP; P16471; 1BP3.
InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor_L_F2.
InterPro; IPR003531; Hematopo_receptor_S_F1.
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
SEQUENCE 896 AA; 102489 MW; D371C7A4186DEEF3 CR
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GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA
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TISSUE-LIVER;

MEDLINE-96206286; PubMed-8616721;

Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-
Platika D., Snodgrass H.R.;

"Novel B219/OB receptor isoforms: possible role
hematopoiesis and reproduction.";
Nat. Med. 2:585-589(1996).

EMBL; U52912; AAC50509.1; -.
HSSP; P16471; 1BP3.
InterPro; IPR003961; FN_III.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor_L_F2.
InterPro; IPR003529; Hematopo_receptor_S_F1.
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
Signal; Receptor.
SIGNAL 1 21 POTENTIAL.
CHAIN 22 958 AA; 109419 MW; C7E0EBD18428677
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Q1-NOV-1996 (TrembLrel. 01, Created)
Q1-NOV-1996 (TrembLrel. 01, Last sequence update)
Q1-NOV-1996 (TrembLrel. 19, Last annotation update)
Q1-DEC-2001 (TrembLrel. 19, Last sequence update)
Q1-NOB RECEPTOR ISOFORM HUB219.1 PRECURSOR.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebratu; Eumammalia; Eutheria; Primates; Catarrhini; Hominidae; Hucheria; Primates; Catarrhini; Hucheria; Primates; Primates; Catarrhini; Primates;                                                                                301
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les 901; Conservative
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Pred. No. 0;
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hini; Hominidae; Homo.
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BD18428677B CRC64;
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Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID-9606;
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SEQUENCE FROM
TISSUE-LIVER;
                                                                                                   TISSUE-LIVER;
MEDLINE-96206286; PubMed-8616721;
Cioffi J.A., Shafer A.W., Zupancic
Platika D., Snodgrass H.R.;
"Novel B219/OB receptor isoforms: I
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MW; 6D51126F33076626 CRC6
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                                                                                           PIFMEGVGK2KIINSFTQDDIEKHQSDA 840
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                                                                     DVPNPKNCSWAQGLNFQK--PETFEHL
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Best Local Similarity 99.7%;
Matches 888; Conservative
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SEQUENCE FROM N.A.
TISSUE-LIVER;
MEDLINE-96206286; PubMed-8616721;
Cioffi J.A., Shafer A.W., Zupancic T.J., Smith Platika D., Snodgrass H.R.;
"Novel B219/OB receptor isoforms: possible rol hematopoiesis and reproduction.";
Nat. Med. 2:585-589(1996).
EMBL; U52914; AAC50511.1; -
HSSP; P16471; 1BP3.
InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor_L_F2.
InterPro; IPR003531; Hematopo_receptor_S_F1.
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
PROSITE; PS01355; HEMATOPO_REC_L_F2; UNKNOWN_1 PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1 Signal; Receptor.
SIGNAL 1 21 POTENTIAL.
CHAIN 22 896 B219/OB RECEPTOR SEQUENCE 896 AA; 102516 MW; 73C431F8C578CD
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                              RYAELYVIDVNINISCETDGYLTKMTCRWSTSTIQ$LAESTLQLRYHRSSLYCSDIPSIH
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B219/OB RECEPTOR ISOFORM
MW; 73C431F8C578CD07 CRC64
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pred. No. 0;
2; Mismatches
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Catarrhini;
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                                                                                                             Query Match 76.1%;
Best Local Similarity 75.3%;
Matches 878; Conservative 1
                                                                                                                                                                "Hyperinsulinemia and leptin receptor variant Ashyperinsulinemic KK mouse strain.";
J. Endocrinol. 21:337-345(1998).
EMBL; Y10296; CAA71342.1; -.
HSSP; P16471; 1BP3.
MGD; MGI:104993; Lepr.
InterPro; IPR002996; CR1A.
InterPro; IPR003529; Hematopo_receptor_L_F2.
InterPro; IPR003529; Hematopo_receptor_S_F1.
InterPro; IPR003529; Hematopo_receptor_S_F1.
Pfam; PF00041; fn3; 3.
SMART; SM00060; FN3; 3.
SMART; SM00060; FN3; 3.
PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1
PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1
Receptor.
VARIANT 600 600 N -> D.
SEQUENCE 1162 AA; 130787 MW; 541E77CBB46EC
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Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI_TaxID=10090;
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Q9QWG3;
Q1-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
LEPTIN RECEPTOR B.
LEPR OR LEPRB.
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ynathi; Muridae; Murinae; Mus
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Becker W., Horborg L.,
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XX MEDLINE-98408931; PubMed-9738551;
XX MEDLINE-SSION In the adipose tissue of normal, hyperinsulinemic, and mrNA

YZ CHARLESSION In the adipose tissue of normal, hyperinsulinemic, and type

YZ diabetic rhesus monkeys.";
XX MEDLINE-ADIPOSE TISSUE;
XX MEDLINE-PROMEDSE TISSUE;
XX MEDLINE-PROMEDSE TISSUE;
XX SEQUENCE FROM N.A.
XX SEQUENCE FROM N.A.
XX SEQUENCE FROM N.A.
XX SUBMITTED ADIPOSE TISSUE;
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XX SUBMITTED ADIPOSE TISSUE;
XX SEQUENCE PROMEDSE TISSUE;
XX SMART; SMONGAC; FN3; 1.
XX SMART; SMONGAC; FN3; 1.
XX PROSITE; PSO1353; HEMATOPO_REC_L_F2; UNKNOWN_1.
XX RECEPTOR.
XX RECEPTOR.
XX SEQUENCE 925 AA; 105721 MW; EC09C27EC29C5F3A CRC64;
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Q9MYK9;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
LEPTIN RECEPTOR SHORT INSERT ISOFORM.
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Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
Cercopithecinae; Macaca.
NCBI_TaxID=9544;
[1]
SEQUENCE FROM N.A.
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nce, tissue distribution, and mRNA
normal, hyperinsulinemic, and type
                                               FFNLNETKPRGKFTYDAVYCCNEHECHH 420
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i; Cercopithecidae;
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C Q9MYL1;
T 01-OCT-2000 (TrEMBLrel. 15, Created)
T 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
T 01-OCT-2000 (TrEMBLrel. 19, Last annotation update)
T 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
E LEPTIN RECEPTOR SHORT ISOFORM.

S Macaca mulatta (Rhesus macaque).

C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
C Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
C Cercopithecinae; Macaca.

X CBI_TaxID=9544;

N [1]
SEQUENCE FROM N.A.

P SEQUENCE FROM N.A.

P SEQUENCE FROM N.A.

TISSUE-ADIPOSE TISSUE;
ANA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C
MONKey leptin receptor mRNA: sequence, tissue distribution, and
expression in the adipose tissue of normal, hyperinsulinemic, and
2 diabetic rhesus monkeys.";
NL Obes. Res. 6:353-360(1998).
                               SEQUENCE FROM N.A.

TISSUE-ADIPOSE TISSUE;
HOTTA K., Gustafson T.A., Ortmeyer H.K., Bodking Submitted (JAN-2000) to the EMBL/GenBank/DDBJ (EMBL; AF225873; AAF35387.1; -. HSSP; P16471; 1BP3.

InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor_L_F2.
InterPro; IPR003531; Hematopo_receptor_S_F1.

Pfam; PF00041; fn3; 2.

SMART; SM00060; FN3; 1.

PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1

PROSITE; PS01355; HEMATOPO_REC_L_F2; UNKNOWN_1
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PROSITE;
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RESULT 13

Q9MZS2

ID Q9MZS2 PRELIMINARY; P
AC Q9MZS2;
DT 01-OCT-2000 (TremBLrel. 15, Cre
DT 01-OCT-2000 (TremBLrel. 15, Las
DT 01-DEC-2001 (TremBLrel. 19, Las
DE TRANSMEMBRANE LEPTIN RECEPTOR (

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Last sequence
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OR (FRAGMENT).

sequence update)
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Query Match 63.5%;
Best Local Similarity 86.5%;
Matches 735; Conservative
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Submitted (JUL-1999) to the EMBL/GenBar EMBL; AF167719; AAF89633.1; -.
HSSP; P16471; 1BP3.
InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor_InterPro; IPR003531; Hematopo_receptor_Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 2.
PROSITE; PS01355; HEMATOPO_REC_L_F2; UPROSITE; PS01355; PS013
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43; Mismatches
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Q1-NOV-1996 (TrEMBLrel. C
Q1-DEC-2001 (TrEMBLrel. 1
LEPTIN RECEPTOR.
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InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematop
InterPro; IPR003531; Hematop
InterPro; IPR003531; Hematop
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
PROSITE; PS01353; HEMATOPO_R
PROSITE; PS01355; HEMATOPO_R
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SEQUENCE
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
[11
                                                                                                                                                                                                                                                                                                                                               STRAIN-SPRAGUE-DAWLEY; Wang M.-Y., Unger R.H.; "Characterization of le
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Submitted (MAR-1996) to the
EMBL; U53144; AAB03088.1; -
HSSP; P16471; 1BP3.
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                                                RNYNYKVHLLYVLPEVLEDSPLVPQKGS 180
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DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE LEPTIN RECEPTOR.
GN 0B-R.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris
OX NCBL_TaxID=9103;
RN [1]
RR SEQUENCE FROM N.A.
RC TISSUE—BRAIN;
RA Richards M.P., Poch S.M., Ashwell C.M.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF321982; AAG40323.1; -.
DR HSSP; P40189; 1BQU.
DR InterPro; IPR002996; CRIA.
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TO SMART; SM00060; FN3; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLL--DFLHVAAAQCMVHEIHPRSFTLPCLLI
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nilarity 48.6%;
Conservative 19
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                                   /TKALKQDDTQDFSAIDSTFTKTEDSEHDSACPSSHFSG
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Pred.
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| |:|||||||:||: || | |
| ALLLWSSLQLRYHRSKIYCSNFPSTPPE 474
                                                                                                                                                                                                                                                                                                                                                                 NLNETKPRGKFTYDAVYCCNEH-ECHHRY 422
|| ||||| | :|:|||::: ||||||||
NLKATKPRGSFFSNALYCCHQNRECHHRY 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YKVHLLYVLPEV-LEDSPLVPQKGSFQMV 184
:||||| : || |||:
MRVHLLYAVSEVSLEDTSTSSLSRTALAA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      790.5; DB 13; Length 1147;
O. 1.9e-197;
atches 364; Indels 45; Gaps
                                                                     DVGNHTKFTFLWTEQAHTVTVLAINSIGA 722
                                                                                                                                                                                                                                                                                                                                                                                                     YFPTKILTSVGSNVSFHCIYKNKTKSVAS
                                                                                                                                                                                                                                                                                                                                                                                                              YFPPKILTSVGSNVSFHCIYKKENKIVPS 363
                                                                                                                                                                                                                                                                                                                                                                                                                                        NPGQNGWQVVQVALNTSLDVDSMLLDSSS 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSTTVIREADKIVSATSLLVDSILPGSSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCSLYRGNMQARMLIPSDISISASEERDS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LNET---SLSPSANGVVQSWSGMRREYGT 65
                                                    MPTTVVSLLS-TTDLEKGSVCISDQFNS 961
                                                                                                                                              /ILTWTLSPQIYVITSLIIEWRNLNKEEE
                                                                                                                                                                                  CVDKGTTCSFPWTEHTHTITILAVNSIGA 713
                                                                                                                                                                                                                               MDIKVPMRGPEFWRIINGDTMKKEKNVTL
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                                                                                                                                                       /IVSWILSPSDYK: MYFIIEWKNLNEDGE 782
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Sear	뮍	Qy	Db	Qy	ф	Qy
Search completed: May 18, 2002, 07:01:59	1121 SIKAIVPYVPQFQMTAAKVQETTEN 1145	1134 SKKTFASYMPQFQTCSTQTHKIMEN 1158	1066 RGLCYLGITSLDKRENAIFLIESSRLMCHFHTADLLRGVGFLQNTPPNLNAFLQS 1120	1075 KSIYYLGVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNIN-LGTS 1133	1011 GVCSGSSWELGSEEFLLLPDQPGSRPCKTLSLISSEGFSEPSDQDDAFTDGGSPE 1065	1022 DSFSNSSWEIEAQAFFILSDQHPNIISPHLTFSEGLDELLKLEGNFPEENNDK 1074

Olden Why IR Joyd SIHL

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Result
No.
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Perfect score:
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution:
 6254
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                                                                                                                                                                                                                                                      Score
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seq length: 2000000000
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92.9
77.3
77.2
77.2
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Match
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2: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
4: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
5: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
6: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
7: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
8: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
9: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1988.DAT:*
10: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*
11: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
12: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
13: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*
14: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*
15: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
16: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
18: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copyright
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AAW24051
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1053.840 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ...QTCSTQTHKIMENKMCDLTV 1165
                                                                                                     Obesity receptor
Human Ob receptor
Peptide Seq ID No:
Peptide Seq ID No:
Human Ob receptor.
Human ob-receptor
Obesity receptor C
Human WSX receptor
Human WSX receptor
Obesity receptor A
                                                                                                                                                                                                                                                        Description
                                                                                                                                                                 Human WSX receptor
Human Ob receptor
Obesity receptor D
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Murine WSX recepto	AAW24054	18	783	50.3	3143
C,	AAW22106	18		53.4	3340
Murine leptin rece	K)	18	842		3479
tein	AAW37338	18	894		3781
Murine short form	AAE12608	22	894	•	œ
Murine short form	AAW19114	18	894		8
Murine WSX recepto	AAW24064	18	894		œ
rece	AAW34258	18	895	60.6	3787
. Ob protein recepto	AAW37337	18	894		α
Rat ob receptor is	AAW34260	18	892	•	œ
	AAW22105	18	900		79
receptor i	AAW34259	18	1015	٠	•
, H	AAW34501	18	804	٠	ű
receptor	AAY05701	20	815	•	Δ
Obesity receptor p	AAW34502	18	839	٠	4554
Human ob-receptor	AAW62543	19	883	٠	1.5
Peptide Seq ID No:	AAY13473	20	1162	76.2	4766.5
	AAE12615	22	1162		\sim
∌	AAW19115	18	1162	٠	\sim
Rat ob receptor (f	AAW23399	18	1162	٠	4778.5
ob receptor	AAW23398	18	1162	•	2
Rat wild-type ob r	AAW34257	18	1162	76.5	4
Human haemopoietin	AAW14841	18	896	٠	~J
1	AAW19536	18	908	•	4799
	AAR88912	17	868		4811
Haematopoietin rec	AAR88911	17	908	•	4813
Human OB-R variant	AAW50002	18	904	٠	$\mathbf{\alpha}$
Human OB-R variant	AAW50003	18	968	77.0	œ
Haematopoietin rec	AAR88910	17	960	•	j
Human haematopoiet	AAW2277,3	18	958	•	ò
OB-R lept	AAW19535	18	958	77.1	19
Human OB-R leptin	AAW31911	18	ū		19
В-	AAW38214	18	958	77.1	4819.5
ecept	AAW34498	18	9		œ

ALIGNMENTS

RESULT

AAW24051 standard;

Protein;

1165

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17-MAR-1998

(first entry)

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AAW24051
ID AAW3
XX
AC AAW3
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AC AAW3
XX
DT 17-N
XX
DE Huma
XX
Huma
KW Huma
KW 1198
KW Carc
KW hype
KW hype
XX
OS Home
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PN W091
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PD 17-1
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PF 07-1
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PR 08-1
PR 08-1
PR 08-1
PR 08-1
Rod1
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Rod1
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XX
Benr
                                                                                                                                                                                                                                                          Human; WSX receptor; variant 13.2; id
ligand; activator; antibody; agonist;
differentiation; anaemia; treatment;
                                                                                                                                                                                                          cardiovascular disease; osteoarthritis hypertension; insulin resistance; hypertriglyceridaemia; cancer; choleli
                                                                                                                                                                                                                                                 Type
                                                                                                           07-JAN-1997;
                                                                                                                                                                                                                                                                                                           Human WSX receptor variant
                       Bennett B,
                                                                        20-JUN-1996;
08-JAN-1996;
                                                                                                                                                             W09725425-A1.
                                                                                                                                                                                    Homo sapiens.
                                                                                                                                    17-JUL-1997.
            Rodrigues
                                               (GETH ) GENENTECH INC
                                                                                                                                                                                                                                               II diabetes; polycystic ovarian
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                         Carter PJ,
                                                                        96US-0667197.
96US-0585005.
                                                                                                            97WO-US00325.
                       Chiang
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                          NY,
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; proliferation; obesity;
neoplasia; arteriosclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is the human WSX receptor variant 13.2, which can be used to identify and purify ligands and activators. An anti-WSX receptor antibody can be used as an agonist to activate the WSX receptor, leading to enhanced proliferation or differentiation of a cell expressing the WSX receptor. It can also be used to decrease body weight and/or fat-depot weight and/or food intake in an obese mammal. WSX receptor ligands can be used to erythroid blood cell lineages. This is useful when a mammal, captured a human, is suffering from decreased blood cell levels, i.e. anaemia, caused by chemotherapy, radiation therapy or bone marrow transplantation therapy. It can also be used to repopulate blood cells in a mammal. The products can also be used to treat, polycystic ovarian disease, cardiovascular diseases, osteoarthritis, dermatological disorders, hypertension, insulin resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer and cholelithiasis.
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 1165; Conser
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haematopo
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N-PSDB;
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                            GSSYEVQVRGKRLDGPGIWSDWSTPRVETTQDVIYFPPKILTSVGSNVSFHCIYKKENKI
                                                                                                                                                                                                                                                                                                                                                   SSVKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV
                                                                   1997-372864/34.
)B; AAT85575.
                                                                                                                                                                                        Pages 81-85;
                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
llarity 100.0%;
Conservative 0
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Pred. No. 0;
Mismatches
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RESULT 2
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AC AAE12609;
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DT 03-JAN-200
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DE Human; ob:
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CS Homo sapic
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FH Key
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FT Protein
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28-DEC-1996;
22-JAN-1996;
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body weight. The invention also relates to a method of identifying therapeutic compounds for the treatment of a body weight disorder. The method involves contacting a cell that expresses a mammalian ObR protein, a JAK2 protein and a mammalian SOCS-1 protein with a test compound. The method is useful for identifying compounds which modulate ObR gene expression and gene product activity, which can be used as agents to control body weight particularly as therapeutic agents for treating body weight disorders, including obesity, cachexia and anorexia.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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08-DEC-1995;
11-DEC-1995;
28-DEC-1995;
22-JAN-1996;
26-APR-1996;
03-SEP-1996;
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Identifying anorexia or protein, cachexia, JAK2 for treating bod comprises contac protein and mam body weight disorder, e.g. obesity, ntacting cell expressing mammalian Ob mammalian SOCS-1 protein with test

Disclosure; Page 109pp; English. . -

The method involves contacting a protein, a JAK2 protein and a man compound. The method is useful for ohr gene expression and gene prodagents to control body weight par treating body weight disorders, if the present sequence is human Observed. The patent encoding th encoding them. ObR protein participate body weight. The invention also relate therapeutic compounds for the treatmen Note: discloses S obese pese receptor (ObR) proteins and nucleic acids in participates in the regulation of mammalian ion also relates to a method of identifying for the treatment of a body weight disorder. Itacting a cell that expresses a mammalian ObR and a mammalian SOCS-1 protein with a test useful for identifying compounds which product ObR particul for identifying compounds which modulate oduct activity, which can be used as articularly as therapeutic agents for including obesity, cachexia and anorexia. ein mutant (Yll41F). he specification but is derived

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The invention provides a method for identifying modulators of binding of CC a phosphorylated leptin receptor with tyrosine phosphatase ID PTP-ID). CC The method comprises: (a) contacting a tyrosine-985 phosphorylated leptin receptor or its phosphorylated fragment with protein PTP-ID or its fragment in the presence and absence of a candidate agent under CC conditions in which in the absence of the agent the binding of the phosphorylated leptin receptor or fragment with PTP-ID or its fragment CC can be detected; and (b) detecting the binding of the phosphorylated CC leptin receptor and PTP ID; where an increase in binding detected in the presence of the agent, indicates that the agent enhances binding, and a decrease in binding in the presence of the agent indicates that the agent is a binding inhibitor. Modulators of tyrosine-985-phosphorylated leptin receptor-dependent PTP-ID phosphorylation are useful as drugs in weight CC content of animals, particularly in mammals. Disorders that can be treated by PTP-ID modulators include obesity and its associated diseases, associated with cancer and AIDS. Additionally the agents identified may be useful in agriculture where body weight of domestic animals can be
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04-DEC-1995;
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11-DEC-1995;
28-DEC-1995;
22-JAN-1996;
26-APR-1996;
                Human Ob receptor (ObR) (AAW19116) is a novel polypeptide that participates in the control of body weight and which is involved in signal transduction triggered by the binding of its natural ligand, Ob (leptin). It is a member of the class I cytokine receptor family. Its amino acid sequence was deduced from a foetal brain cDNA clone (AAT69592). The receptor corresponds to the long form mouse ObR (AAW19115). ObR proteins, peptides, antibodies, agonists and antagonists can be used in the diagnosis and treatment of body weight disorders such as obesity, cachexia and anorexia.
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Sequence
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N-PSDB; AAT69592.
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N-PSDB; AAT98530.
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08-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 77.2%;
Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                              Claim
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N-PSDB; AAT98528.
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N-PSDB;
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Also described is the use of labelled DNA probes based on the OB-R sequence to screen for other variants.
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N-PSDB;
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clibrary. The sequence shows near identity to a published OB-R sequence in the extracellular domain, with the exception of 3 amino acids, but there is extensive diversity in the intracellular cytoplasmic domain at the C-terminal end. A claimed method for Cytoplasmic domain at the C-terminal end. A claimed method for detection of OB-R in cells comprises extraction of: RNA and testing this for hybridisation to an oligonucleotide (I) derived from the COB-R variant gene, especially from the region beyond nucleotide administration of an agent that inhibits expression of the OB-R variant gene; and (2) identification of a compound that can supplement activity of leptin by: (I) incubating cells expressing OB-R variant first with leptin and then with a test compound, and (i) comparing activation signals between cells treated and not treated with the test compound. Inhibition/down-regulation of the variant OB-R (found in obese people) improves response of cells to weight regulation by leptin. Replacing variant OB-R by gene therapy (in homozygous individuals) can be used to treat obesity. Labelled probes based on the gene can be used to isolate other variant forms of the receptor gene or to detect the variant gene (e.g. for determining predisposition to obesity), while the OB-R gene can be used to express recombinant OB-R (optionally as fusion protein) and in standard hybridisation assays. The OB-R gene can also be used the rapeutically in cases of overexpression of functional OB-R (causing loss of appetite and hypermetabolic activity). Cells cartibodies that competitively inhibit, neutralise or enhance activity of the variant receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This polypept (OB-R). Its derived from
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Similarity 94.1%;
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Pred. No. 0;
7; Mismatches
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Query Match Best Local S Matches 901

cch 77.1%; il Similarity 94.1%; 901; Conservative

Score 4819.5;
Pred. No. 0;
7; Mismatches

. 4819.5; No. 0;

DB 18;

Length 958;

25; Indels 25; Gaps

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cc detection of a common precursor mRNA. A claimed method for this for hybridisation to an oligonucleotide (I) derived from the CC OB-R variant gene, especially from the region beyond nucleotide CZ 2770. Also claimed are methods of: (1) treating obesity by CC administration of an agent that inhibits expression of the OB-R CC variant gene; and (2) identification of a compound that can CC supplement activity of leptin by: (1) incubating cells expressing CC OB-R variant first with leptin and then with a test compound, and CC (ii) comparing activation signals between cells treated and not treated with the test compound. Inhibition/down-regulation of the CC variant OB-R (found in obese people) improves response of cells to comparing activation to be used to treat obesity. Labelled CC weight regulation by leptin. Replacing variant OB-R by gene therapy (in homozygous individuals) can be used to treat obesity. Labelled CC of the receptor gene or to detect the variant gene (e.g. for CC determining predisposition to obesity), while the OB-R gene can be used to express recombinant OB-R (optionally as fusion protein) and compended to express variant observes of functional OB-R (causing loss of appetite and hypermetabolic activity). Cells creen for (ant)agonists of leptin/OB-R interaction, also to generate CC antibodies that competitively inhibit, neutralise or enhance activity X
cytoplasmic domain at the C-terminal en-
splicing of a common precursor mRNA. A
detection of OB-R in cells comprises ex-
this for hybridisation to an oligonucle
OB-R variant gene, especially from the
2770. Also claimed are methods of: (1)
administration of an agent that inhibit,
variant gene; and (2) identification of
supplement activity of leptin by: (i) if
OB-R variant first with leptin and then
(ii) comparing activation signals between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence in the extracellular domain, acids, but there is extensive diversi
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting defective form of leptin re - with oligonucleotide derived from D treatment of obesity by inhibiting ex and screening for agents that increas
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DB; AAT72649.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide comprises a variant of the human leptin receptor its sequence was deduced from a contiguous cDNA (AAT72649) com overlapping clones isolated from a human foetal liver. The sequence shows near identity to a published OB-R
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DNA of receptor variant, also
expression of variant receptor
se leptin activity
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Search completed: May Job time: 5693 sec 2002, 06:52:53

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1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US080_COMB.pep:*

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20: /cgn2_6/ptodata/1/paa/US094_COMB.pep:*

21: /cgn2_6/ptodata/1/paa/US095_COMB.pep:*

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ALIGNMENTS

RESULT 1
US-08-570-142D-4
; Sequence 4, Application US/08570142D
; GENERAL INFORMATION: CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatibl
OPERATING SYSTEM: Windo SOFTWARE: FastSEQ for Windows Versi CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/570,142D FILING DATE: 11-DEC-1995 PRIOR APPLICATION DATA: APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING
TITLE OF INVENTION: OBESITY AND CACHEXIA CORRESPONDENCE ADDRESSEE: F APPLICANT: NUMBER OF SEQUENCES: APPLICATION NUMBER: 0 FILING DATE: 08-DEC-1 APPLICATION NUMBER: 0 225 Tartaglia, Louis, Tepper, Robert I. DE ADDRESS:
Fish & Richardson,
Tranklin Street IBM Compatible Windows 95 08/569,485 C-1995 08/566,622 > שׁ O lon 2.0

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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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Best Local Similarity 100.0%;
Matches 1165; Conservative 0;
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APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/014001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-8906
TELEFAX: 617-542-8906
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TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
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Pred. No. 0;
Mismatches
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GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

APPLICANT: Tepper, Robert I.

APPLICANT: Culpepper, Janice A.

TITLE OF INVENTION: THE OB RECEPTOR AN

TITLE OF INVENTION: DIAGNOSIS AND TREA

TITLE OF INVENTION: OBESITY AND CACHEX

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,15:
FILING.DATE: 28-DEC-1995
PRIOR APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
APPLICATION NUMBER: 35,283
REGISTRATION NUMBER: 35,283
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/0:
                                                                                                                                                                                                                                                                                                                                                    STREET: 225 Franklin St
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMMPTTVVSLLSTTDLEKGSVCISDQFN 960
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28-DEC-1995
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; TELEX: 20(
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; LENGTH: 1:
; TYPE: amii
; TOPOLOGY:
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; FRAGMENT TYPI
US-08-583-153A-4
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TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
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Best Local Similarity
Matches 1165; Conserv
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FRAGMENT TYPE:
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TOPOLOGY: unknow
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GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED
GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED
                                                                             TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
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Pred. No. 0;
Mismatches
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NUMBER OF CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,005
FILING DATE: 08-Jan-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-585-005-2
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US-08-585-005-2
; Sequence 2, Application
; GENERAL INFORMATION:
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MICQKECVVLLHWEE IYVITAFNLSYPITPWRE
                                              cal Similarity 100.0%;
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KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMMPTTVVSLLSTTDLEKGSVCISDQFN 960
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                                                   Score 6254;
Pred. No. 0;
Mismatches
FKLSCMPPNSTYDYFLLPAGLSKNTSNS 60
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KDSFSNSSWEIEAQAFFILSDQHPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIYYL KDSFSNSSWEIEAQAFFILSDQHPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIYYL
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GLYVIVPVIISSSILLLGTLLISHQRMKKLFWEDVPNPKNCSWAQGLNFQKPETFEHLFI
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APPLICANT:
APPLICANT: Colpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND M
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TITLE OF INVENTION: THE OB RECEPTOR AND M
TITLE OF INVENTION: THE OB RECEPTOR AND M
TITLE OF INVENTION: THE OB RECEPTOR AND M
TITLE OF INVENTION: THE OB RECEPTOR AND TITLE OF INVENTION: CACHEXIA

NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: BOSTON
STREET: WAA
COUNTRY: BOSTON
STREET: WAS COUNTRY: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskettle
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskettle
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskettle
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETING
OMPUTER READABLE FORM:
MEDIUM TYPE: DISKETING
OMPUTER READABLE FORM:
MEDIUM TYPE: OBATA:
APPLICATION NUMBER: 08/08/638,524B
FILING DATE: 22-JAN-1996
PRICH APPLICATION NUMBER: 08/59,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/56,485
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/56,485
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/56,485
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/56,622
APPLICATION NUMBER: 08/56,622
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US-08-638-524B-4
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Best Local Similarity 100.0%;
Matches 1165; Conservative 0
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                            GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFAS
                                                        KDSFSNSSWEIEAQAFFILSDQHPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIYYL KDSFSNSSWEIEAQAFFILSDQHPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIYYL
                                                                                     KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMMPTTVVSLLSTTDLEKGSVCISDQFN
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GENERAL INFORMATION:
APPLICANT: Matthews, William
TITLE OF INVENTION: USES FOR WSX LIGA
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb flo
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION NUMBER: US/08/667,197
FILING DATE: 20-Jun-1996
CLASSIFICATION ATA:
APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: P-40,378
REFERENCE/DOCKET NUMBER: P0986P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
TELEFAX: 415/952-9881
TELEFAX: 415/952-9881
TELEFAX: 415/952-9881
TELEFAX: 415/952-9881
TELEFAX: 415/952-9881
TELERGTH: 1165 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-667-197-2
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APPLICANT: Matthews
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                         QQIDANWNIQCWLKGDLKLFICYVESLFKNLFRNYNYKVHLLYVLPEVLEDSPLVPQKGS 180
QQIDANWNIQCWLKGDLKLFICYVESLFKNLFRNYNYKVHLLYVLPEVLEDSPLVPQKGS 180
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1165; Conser
VPSKEIVWWMNLAEKIPQSQYDVVSDHVSKVT
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larity 100.0%;
Conservative
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Pred. No. 0;
Pred. No. 0;
Mismatches
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                         TYFPPKILTSVGSNVSFHCIYKKENKI 360
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FNLNETKPRGKFTYDAVYCCNEHECHH
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US-08-708-123D-4
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                   APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
APPLICANT: White, David W.
FITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                     Sequence 4, Application US/08708123D GENERAL INFORMATION:
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STREET: 225 F
CITY: Boston
STATE: MA
COUNTRY: US
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                                                                   BODY
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Query Match
Best Local Similarity
Matches 1165; Conserv
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 07-S66,622
FILING DATE: 27-NOV-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/01900
TELEPHONE: 617-542-8906
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 200154
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: D1skette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows V.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: prote
                                                                                                                                                                                                             LGLHMEITDDGNLKISWSSPPLVPFPLQYQVI
                                                                                                                                                          100.0%;
nilarity 100.0%;
Conservative 0;
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RESULT 7
US-08-779-457-2
; Sequence 2, Application US/08779457
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Chiang, Nancy Y.
; APPLICANT: Kyung, Jin Kim
; APPLICANT: Matthews, William
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                    APPLICANT: Matthews, William
APPLICANT: Rodrigues, Maria L.
TITLE OF INVENTION: WSX RECEPTOR AG
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
ADDRESSEE:
STREET: 46
CITY: SOUT.
STATE: Cal
COUNTRY: U.
ZIP: 94080
COMPUTER READ
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GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED
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READABLE
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TYPE: Amino Acid
TOPOLOGY: Linear
US-08-779-457-2
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REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P098
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEY: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667197
FILING DATE: 06/20/96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
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LGLHMEITDDGNLKISWSSPPLVPFPLQYQVKYSENSTTVIREADKIVSATSLLVDSILP 300
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1165; Conserv
SSYKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV 600
SSYKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV 600
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NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
                                                        PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWI
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Pred. No. 0;
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Sequence 2, Application US/08780562

GENERAL INFORMATION:

APPLICANT: Matthews, William

APPLICANT: Bennett, Brian

TITLE OF INVENTION: WSX RECEPTOR

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy dis

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/780,562

FILING DATE:

CLASSIFICATION DATA:

APPLICATION NUMBER: 08/585005

FILING DATE: 01/08/97

PRIOR APPLICATION NUMBER: 60/

FILING DATE: 01/08/97

ATTORNEY/AGENT INFORMATION:
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US-08-780-562-2
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GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED
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REFERENCE/DOCKET NUMBER: P098
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-780-562-2
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Best Local Similarity
Matches 1165; Conser
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                                                                                                  PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTV
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                          GASVANFNLTFSWPMSKVNIVQSLSAYPLNSS
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FR: P0986R1
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red. No. 0;
Mismatches
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                                                              CLKITSGGVIFQSPLMSVQPINMVKPDPP 240
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US-09-094-410-4
; Sequence 4, Application:
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                                            SOFTWARE: FASTSEQ for Windows Versic CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/094,410
FILING DATE: 09-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
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TITLE OF INVENTION: T
TITLE OF INVENTION: T
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APPLICANT: T
APPLICANT: (
APPLICANT: (
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STREET: 225 F1
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-28
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                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: Windows SOFTWARE: Faster
APPLICATION NUMBER: 08/566,622 FILING DATE: 04-DEC-1995 APPLICATION NUMBER: 08/562,663 FILING DATE: 27-NOV-1995
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Fish & Ri
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; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protei
; FRAGMENT TYPE: intern
US-09-094-410-4
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Best Local Similarity
Matches 1165; Conserv
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REFERENCE/DOCKET NUMBER: 0733.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
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LENGTH: 1165 amino acids
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GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780 GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780
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                                              RYAELYVIDVNINISCETDGYLTKMTCRWSTST
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FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCI
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llarity 100.0%;
Conservative
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Pred.
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Gaps

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RESULT 10
US-09-137-132-4
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SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/137,132
FILING DATE: 18-AUG-1998
PRIOR APPLICATION NUMBER: 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/569,485
PILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
PILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/569,485
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: White, David W.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF I
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
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APPLICANT: 7
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MEDIUM TYPE: Diskette
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CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
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YMPQFQTCSTQTHKIMENKMCDLTV 1165
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Culpepper, Janice A.
White, David W.
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
TOPOLOGY: unknown
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Best Local Similarity
Matches 1165; Conser
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FRAGMENT TYPE:
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REFERENCE/DOCKET NUMBER: 07334/019
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/50
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
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          TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWS
                                                         PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
                                                                                         SSVKAEITINIGLLKISWEKPVFPENNLQFQI
                                                                                                                                       VPSKEIVWWMNLAEKIPQSQYDVVSDHVSKVT
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                                              PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYT
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Pred. No. 0;
Mismatches
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                                                                                         RFKLSCMPPNSTYDYELLPAGLSKNTSNS 60
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SEDVGNHTKETELNTEQAHTVTVLAINSI 720
                                               /VMDIKVPMRGPEFWRIINGDTMKKEKNV
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Gaps

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RESULT 11
US-09-950-149-4
; Sequence 4, Application US/09950149
; GENERAL INFORMATION:
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COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Versic
SOFTWARE: FastSEQ for Windows Versic
APPLICATION NUMBER: US/09/950,149
FILING DATE: 10-Sep-2001
PRIOR APPLICATION NUMBER: 09/069,781
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: US 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: US 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: US 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: US 08/570,142
FILING DATE: 11-DEC-1995
                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish &
                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
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GASVANFNLTESWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED
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                                                                                                                                                                                                                                                                                                                CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Fish & Richardson, STREET: 225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                                                                                             INVENTION: THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tartaglia, Louis A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Culpepper, Janice A. White, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tepper,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Robert
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SEQUENCE CHARACTERISTICS:

LENGTH: 1165 amino acid

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ II

US-09-950-149-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 6254; Best Local Similarity 100.0%; Pred. No. 0; Matches 1165; Conservative 0; Mismatches
                                                                               481
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FILING DATE: 08-DEC-1995
APPLICATION NUMBER: US 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/08
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 542-5070
TELEFAX: 200154
TELEX: 200154
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                                                                                                                                                                       LGLHMEITDDGNLKISWSSPPLVPFPLQYQVKYSENSTTVIREADKIVSATSLLVDSILP 300
                                                                                                                                                                                                                                                                                                                FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP 240
PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
                                            SSVKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV 600
                                 SSVKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV
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RESULT 12
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REFERENCE/DOCKET NUMBER: FINFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 1216 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                            APPLICANT: CHANG, MING-SHI
APPLICANT: WELCHER, ANDREW A.
APPLICANT: FLETCHER, FREDERICK A.
TITLE OF INVENTION: OB PROTEIN RECEPTOR AND REL
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774.414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application:
                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Pessin, Karol M.
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                                                                                                                                                         APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 42
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US-08-774-414-7

DB 11;

Length 1216;

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1 MICQKFCVVLLHWEFIYVITAFNLSYPITPWRFKLSCMPPNSTYDYFLLPAGLSKNTSNS 60 KHTASVTCGPLLLEPETISEDISVDTSWKNKD GASVANFNLTFSWPMSKVNIVQSLSAYPLNSS
GASVANFNLTFSWPMSKVNIVQSLSAYPLNSS GLYVIVPVIISSSILLLGTLLISHQRMKKLFW GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLY TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWS SSVKAEITINIGLLKISWEKPVFPENNLQFQI PISEPKDCYLQSDGFYECIFQPIFLLSGYTMW PISEPKDCYLQSDGFYECIFQPIFLLSGYTMW RYAELYVIDVNINISCETDGYLTKMTCRWSTS VPSKEIVWWMNLAEKIPQSQYDVVSDHVSKVT GSSYEVQVRGKRLDGPGIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCIYKKENKI 360 LGLHMEITDDGNLKISWSSPPLVPFPLQYQVK FQMVHCNCSVHECCECLVPVPTAKLNDTLLMC SVNFSEAEGTEVTYEDESQRQPFVKYATLISN GLYVIVPVIISSSILLLGTLLISHQRMKKLFW GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLY TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWS LGLHMEITDDGNLKISWSSPPLVPFPLQYQVK VPSKEIVWWMNLAEKIPQSQYDVVSDHVSKVT 0 Score 6 Pred. No. NO. 0; SCVIVSWILSPSDYKLMYFIIEWKNLNED IEDVPNPKNCSWAQGLNFQKPETFEHLFI RYGLSGKEVQWKMYEVYDAKSKSVSLPV VIRINHSLGSLDSPPTCVLPDSVVKPLPP (YSENSTTVIREADKIVSATSLLVDSILP 300 LKITSGGVIFQSPLMSVQPINMVKPDPP EMMPTTVVSLLSTTDLEKGSVCISDQFN PIFMEGVGKPKIINSFTQDDIEKHQSDA EDVGNHTKFTFLWTEQAHTVTVLAINSI 720 FFNLNETKPRGKFTYDAVYCCNEHECHH 420 RNYNYKVHLLYVI,PEVLEDSPLVPQKGS SKPSETGEEQGLINSSYTKCFSSKNSPL PIFMEGVGKPKIINSFTQDDIEKHQSDA EDVGNHTKFTFLWTEQAHTVTVLAINSI YSENSTTVIREAUKIVSATSLLVDSILP 0,: Indels 0; Gaps 960 720 180 960 900 900 840 780 600 600 180 840 780 660 660 540 540 240 300 240

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WO: 7:

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WO: 7:

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: prote

SEQUENCE DESCPT

US-09-671-049-7
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US-09-671-049-7
; Sequence 7, Application US/09671049
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; WELCHER, ANDREW A.
; FLETCHER, FREDERICK
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Best Local Similarity
Matches 1165; Conser
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/774,414
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol M.
REFERENCE/DOCKET NUMBER: A-382-A
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1216 amino acids
TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/671,049
FILING DATE: 27-Sep-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE MEDIUM TYPE:
                                                                                          MICQKFCVVLLHWEFIYVITAFNLSYPITPWRFKLSCMPPNSTYDYFLLPAGLSKNTSNS
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                                             KDSFSNSSWEIEAQAFFILSDQHPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIYYL KDSFSNSSWEIEAQAFFILSDQHPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIYYL
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STATE: California
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Pred. No. 0;
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GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED
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YMPQFQTCSTQTHKIMENKMCDLTV
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TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
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RESULT 14 US-09-948-933-284

Sequence GENERAL I

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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES AS:
TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE ANI
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL000787
CURRENT APPLICATION NUMBER: US/09/948,933
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/231,399
PRIOR APPLICATION NUMBER: 60/231,399
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 6404
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 284
LENGTH: 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 1163; Conserv
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TYPE: PRT
ORGANISM: Human
-09-948-933-284
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US-09-948-947-87
; Sequence 87, Application US/09948947
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
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TITLE OF INVENTION: POLYMORPHISMS IN KNC
TITLE OF INVENTION: WITH TYPE II DIABET
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000786
CURRENT APPLICATION NUMBER: US/09/948,94
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 2172
SOFTWARE: FastSEQ for Windows Version 4.
SEO ID NO 87
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                       FQMVHCNCSVHECCECLVPVPTAKLNDTLLMC
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                                                                                       KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMMPTTVVSLLSTTDLEKGSVCISDQFN
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GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED
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Search completed: May 18, 2002, 06:59:12 Job time: 680 sec

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Title: Perfect

Sequence:

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GenCore version (c) 1993 - 2000

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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*
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US-09-935-868-26
; Sequence 26, Application US/09935868
; GENERAL INFORMATION:
APPLICANT: Regeneron Pharmaceuticals, Inc
ITILE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
FILE REFERENCE: REG 203D
CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
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LENGTH: 1158
TYPE: PRT
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PCT-US02-09671-870
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US-09-935-868-44
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PCT-US02-09671-862
PCT-US02-09671-862
PCT-US02-09671-862
PCT-US02-09671-869
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PCT-US02-09671-872
US-09-935-868-30
PCT-US02-07826-219
US-10-097-340-219
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Pred. No. 1.3e-18;
D; Mismatches 441; Indels 244; Gaps
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53;

TWMVKDLQH----HCVIHDAWSGLRH

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-RVFTTQDVI----YFPPKI-LTS

343

348

EPKDCYLQSDGFYECI--FQPIFLLSGY

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--NINISC-ETDGYLTKMTCRWST

--DCKAKRDIPTSCIVDYSTVYFVN-I 503

-IGLEKISWEKP----

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Result

Pred. score and is

QY 196 CLYPVPTAKLNDTLL-MCLKITSGGVIFQSPLMSVQPINMVKPDPPLGLHMEITDDGN 252	Query Match 6.0%; Score 376; DB 5; Length 1168; Best Local Similarity 19.6%; Pred. No. 4.7e-18; Matches 213; Conservative 177; Mismatches 445; Indels 254; Gaps 51;	ЖТ М: н 68-2	NUMBER OF SEQ ID NOS: 52 SOFTWARE: PatentIn version 3 SEQ ID NO 24	URRENT APPLICATION URRENT FILING DATE: RIOR APPLICATION NU RIOR FILING DATE: 1	GENERAL INFORMATION: APPLICANT: Regeneron Pharmaceutica TITLE OF INVENTION: Receptor Based FILE REFERENCE: REG 2010	RESULT 2 US-09-935-868-24 ; Sequence 24, Application US/09935868	Qy 1079 YLGVTSIKKRESGYLLTDKSRVSCPFPAPCLFTDIRVLQDSC-SHFVENNINL 1130	QY 1033 AQAFFILSDQHPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIY 1078 : : : : :	QY 991SNSKPSETGEEQGLINSSVTKCFSSKNSPLKDSFSNSSWEIE 1032 : :	QY 953VCISDQFNSVNFSEAEGTEVTYEDESQRQPFVKYATLI 990 ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	QY 901 KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMMPTTVVSLLSTTDLEKGS 952 	QY 853 SILLIGTLLISHQRMKKLFWEDVPNPKNCSWAQGLN-FQKPETFEHLFI 900	QY 793 KKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDAGLYVIVPVIISS 852 : : : :: : : :	QY 735 MSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNEDGEIKWLRISSSV 792 : : : : : : : : : :	QY 679 YVINHHTSCNGTWSEDVGNHTKETFLWTEQAHTVTVLAINSIGASVANFNLTFSWP 734 ; ; ; ; ; ; ; ; ; ;	Qy 619 LGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNVTLLWKPLMKNDSLCSVQR 678 	QY 562 -VFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPVPDLCAVYAVQVRCKRLDG 618 : : : :: : :: : Db 561 VIILKYNIQYRTKDASTWSQIPPEDTASTRSSFTVQDLKPFTEYVFRIRCMKEDG 615	Db 504 EVWVEAENALGKVTSDHINFDPVYKVKPNPPHNLSVINSEELSSILKLTWTNPSIKS 560
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; SOFTWARE: PatentIn versic
; SEQ ID NO 4
; LENGTH: 918
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-853-180-4; Sequence 4, Application US/09853180; GENERAL INFORMATION:
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Best Local Similarity 19.8
Matches 163; Conservative
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TITLE OF INVENTION: Mammalian Receptor Proteins;
FILE REFERENCE: DX01074
CURRENT APPLICATION NUMBER: US/09/853,180
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,426
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 5
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APPLICANT: Parham, Christi |
APPLICANT: Kastelein, Rober:
APPLICANT: Moore, Kevin W.
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VRMAAYTDEGGKDGPEFTFTTPKFAQGEIEAIVVPVCLAFLLTTLLGVLFCFNKRDLIKK
                                                               GKNEAVLEWDQLPVDVQNGFIRNYTIFYRTIIGNETAVNVDSSHTEYTLSSLTSDT-LYM
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Kastelein, Robert A.
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                               -VIVPVIISSSI-LLLGTLLISHQR--MKK
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Qy	30 NKDEMMPTTVVSLLSTTDLEKGSVCISDQFNSVNFSEAEGTEVTYEDESQRQPFVKY
Db	: : 678 SKDQM
Qy	987 ATLISNSKPSETGEEQGLINSSVTKCFSSKNSPLKDSFSNSS 1028
дb	711 LDLFKKEKINTEGHSSGIGGSSCMSSSRPSISSSDENES 749
RESUL US-09 Seq GEN FIT PR SO SEQ US-09	ULT 4 09-935-868-7 equence 7, Application US/09935868 ENERAL INFORMATION: APPLICANT: Regeneron Pharmaceuticals, Inc APPLICANT: Regeneron Pharmaceuticals, Inc TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using FILE REFERENCE: REG 203D CURRENT APPLICATION NUMBER: US/09/935,868 CURRENT FILING DATE: 2002-04-11 PRIOR APPLICATION NUMBER: PCT/US99/22045 PRIOR APPLICATION NUMBER: PCT/US99/22045 PRIOR FILING DATE: 1999-09-22 NUMBER OF SEQ ID NOS: 52 SOFTWARE: Patentin version 3.0 EQ ID NO 7 LENGTH: 859 TYPE: PRT ORGANISM: Homo sapiens 09-935-868-7
Que Bes Mat	4.9%; Score 309.5; DB 5; Length 859; st Local Similarity 19.6%; Pred. No. 1.3e-13; ches 178; Conservative 145; Mismatches 378; Indels 209; Gaps 42;
Qу	337 PPKILTSVGSNVSFHCIYKKENKIVPSKEIVWWMNLAEKIPQSQYDVVSDHVSKVTF 393 : : : : : :
Qy	394 FNLNETKPRGKFTYDAVYCCNEHECHHRYAELYVIDVNINISC-ETDGYLTK 444
2 Q	445 MTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIHPISEPKDCYLQSDGFYECIFQP 502
δĀ	3 IFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPPSSVKAEITINIGLLKISW
DЪ	YFVN-IEVWVEAENALGKVTSDHINFDPVYKVKPNPPHNLSVINSEEL
Qy	559 EKPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLFVPDLCAVYAVQV 611
Db	RTKDASTWSQIPPEDTASTRSSFTVQDLKPFTEYVFRI
d Q	612 RCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNVTLLWKPLMKND 671
Qy	672 SLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTYTVLAINSIGASVANF 727
} 5	9 ANGKILDYEVILTRWKSHLQNYTVNATKLTVNLTNURYLATUTVKNLVGXSDAAV
g 7	414 LTIPACDEQATHPYMDLKAEP-KDNMLWYEWTTPRESYKKYILEWCYLSDKAPCITDW 470
Qy	786 LRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDAGLYVI 845
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RESULT 5
US-09-935-868-9
: Sequence 9, Application US/09935868
: GENERAL INFORMATION:
: APPLICANT: Regeneron Pharmaceuticals, Inc
: TITLE OF INVENTION: Receptor Based Antagonists,
: FILE REFERENCE: REG 203D
: CURRENT APPLICATION NUMBER: US/09/935,868
: CURRENT FILING DATE: 2002-04-11
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LENGTH: 951
TYPE: PRT
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Best Local Similarity 22.4%;
Matches 117; Conservative 9
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                                                                VYFVN-IEVWVEAENALGKVTSDHINFDPVYKVKPNPPHNLS----VINSEELSSILKLTW
                                                                                                IFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPPSSVKAEITIN---
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RESULT 6
US-09-853-180-5
; Sequence 5, Application US/09853180
; GENERAL INFORMATION:
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SOFTWARE: Pace
SEQ ID NO 5
TONGTH: 862
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Best Local Similarity
Matches 182; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MOOTE, KEVIN W. TITLE OF INVENTION: Mammalian FILE REFERENCE: DX01074
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APPLICANT: Parham, Christi L
APPLICANT: Kastelein, Robert
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                               NYTLLWKPLMKNDSLCSVQRYVINHHTSCNG
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                                                                       EFQISSKLHLYKGSWSDWSES
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llarity 19.8%;
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No. 2e-07;
natches 322;
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                          TWSEDVGNHTKFTFLWTEQAH-TVTVLA 716
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APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE PO
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C1
CURRENT APPLICATION NUMBER: US/10/119,480
CURRENT FILING DATE: 2002-04-09
NUMBER OF SEQ ID NOS: 246
                                                                               Query Match
Best Local
                                                                                                                                                                                             SEQ ID NO 92
LENGTH: 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 92, Application US/10119480 GENERAL INFORMATION:
                                                                 Matches
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                                                                Local Similarity
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                              NISCETDGYLTKMTCRWSTSTIQSLAESTLQLRYHRSSLY--CSDIPSIHPISEPKDCYL
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NISC-VYYYRKNLTCTWSPGKETSYTQYTVKRTYAFGEKHDNCTTNSS
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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                                                             3.5%; Score 218.5;
20.4%; Pred. No. 1.6;
Eve 100; Mismatches
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US-09-935-868-10
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Best Local Similarity
Matches 77; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 10
LENGTH: 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Receptor Based Antagon FILE REFERENCE: REG 203D CURRENT APPLICATION NUMBER: US/09/935,868 CURRENT FILING DATE: 2002-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Regeneron Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
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                                     MTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIHPISEPKDCYLQSDGFYECI--FQP 502
                                                                                                                                                                                               PPKILTSVGSNVSFHCIYKK---ENKIVPSKEI
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Pred. No:
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ed. No: 5.5e-06;
Mismatches 140; Indels 59; Gaps
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                                                                            GITIISGLPPENFKNLSCIVNEG--KK 141
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--HKFA---DCKAKRDTPTSCTVDYST 188
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PCT-US02-09052-7
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NAME/KEY: misc_feature

OTHER INFORMATION: Incyte
PCT-US02-09052-7
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Best Local Sim
Matches 218;
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GENERAL 3
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NUMBER OF SEQ ID NOS: 24

COSTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER:
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TYPE; PRT
ORGANISM: Homo sapiens
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                                                 VIGQDVVLPCVASG---
 > 7, Application PC/TUS0209052
INFORMATION:
                                                                             QKGSFQMVHCNCSVHECCECLVPVPTAK-
                                                                                                                                                                      VYAGN--NAILNCEVNADLVPFVRWEQNRQPLLLDDRVIKLPSGMLVISNAT--
                                                                                                                                                                                                         THESNLSKTTEHC-
                                                                                                                                                                                                                                   LLPDGSLFISNVVHSKHNKPDEGYYQCVATVESLGTIISRTAKLIVAGLPRFTSQPEPSS
                                                                                                                                                                                                                                                                       LLPAGL -
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                                                                                                                                        ANWNIQCWLKGDLKLFICYVESLFKNLFRNYNYKVHLLYVL-PEVLED--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US02/09052 FILING DATE: 2002-03-12
                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                           EGDGGLYRCVVES--
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AN, Brendan M.
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PCT-US02-09671-1148
; Sequence 1148, Application PC/TUS020967:
; GENERAL INFORMATION:
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PRIOR PRIOR PRIOR
                                        APPLICANT: ZYCOS INC.
TITLE OF INVENTION: TRANSLATIONAL PROFIFILE REFERENCE: 08191-026WO1
CURRENT APPLICATION NUMBER: PCT/US02/09
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/279,495
PRIOR FILING DATE: 2001-03-28
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APPLICATION NUMBER: FILING DATE: 2001-0 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             DLFVINAPYTPVPDPTPMMPPVGVQASIL--
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                          60/292,544
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                                                                                                                                                                                                                                                                                                                                               ESOROPEVKYATLISNSKPSET-----
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PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/326,370
PRIOR FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 60/336,780
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/358,985
PRIOR FILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 2041
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 1148
LENGTH: 1461
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                                                                                                    DVAVRTLSDVPSAAPQNLSL----EVRNSKSIMIHWQPPAPATQNGQITGYKIRYRKASR
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 VQ---SLSAYPLNSSCVIVSWILSPSD---
                                                                NGTWSEDVGNHTKFTFL-----WTEQAHTVTVLAINSIGASVANFNL-TFSWPMSKVNI
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Qy 48 LLPAGL	RESULT 11 PCT-USO2-10824-189 ; Sequence 189, Application PC/TUSO210824 ; GENERAL INFORMATION: APPLICANT: OriGene Technologies ; TITLE OF INVENTION: Prostate Cancer Expression Profiles ; FILE REFERENCE: 9U 206 PCT ; CURRENT APPLICATION NUMBER: PCT/USO2/10824 ; CURRENT FILING DATE: 2002-04-08 PRIOR APPLICATION NUMBER: US 60/281,732 ; PRIOR APPLICATION NUMBER: US 60/281,731 ; PRIOR FILING DATE: 2001-04-06 ; NUMBER OF SEQ ID NOS: 211 ; SOFTWARE: Patentin version 3.1 ; SEQ ID NO 189 ; LENGTH: 1461 ; TYPE: PRT ; ORGANISM: Homo sapiens PCT-USO2-10824-189 PCT-USO2-10824-189 Query Match Best Local Similarity 19.6%; Pred. No. 0.0013; Matches 218; Conservative 151; Mismatches 407; Indels 339;	OY 999 -GEEQGLINSSVTKCFSSKNSPLKDSFSNSSWEIE 1032	883QKITDSRYYTVRW	QY 841 GLYVI	Db 739 PEVPSSLHVRPLVTS-IVVSWTPPENQNIVVRGYAIGYGIGSPHAQTIKVDYK Qy 781 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA
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                                                                                                                                                                                                                                                                    Sequence 1147, Application PC/TUS0209671 GENERAL INFORMATION:
                                                                                                                                                                                                              APPLICANT: Zycos Inc.
TITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE REFERENCE: 08191-026WO1
                                                                                       PRIOR APPLICATION NUMBER: 60/292,544 PRIOR FILING DATE: 2001-05-21 PRIOR APPLICATION NUMBER: 60/310,801
                                                                                                                                          PRIOR APPLICATION NUMBER: 60/279,495 PRIOR FILING DATE: 2001-03-28
                                                                                                                                                                               CURRENT APPLICATION NUMBER: PCT/US02/09671 CURRENT FILING DATE: 2002-03-28
                                                                         PRIOR
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APPLICATION
FILING DATE:
                                    APPLICATION NUMBER: 60/310,801 FILING DATE: 2001-08-08 APPLICATION NUMBER: 60/326,370 FILING DATE: 2001-10-01
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Best Local Similarity 19.0
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PRIOR FILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 2041
SOFTWARE: FastSEQ for Windows
SEQ ID NO 1147
LENGTH: 1461
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Pred. No. 0.0013;
1; Mismatches 407;
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PIFMEGVGKPKIINSFTQDDIEKHQSDA 840
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CURRENT APPLICATION NUMBER: PCT/US02/0
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/279,495
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/292,544
PRIOR FILING DATE: 2001-05-21
PRIOR FILING DATE: 2001-08-08
PRIOR FILING DATE: 2001-08-08
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Best Local S
Matches 218
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PRIOR FILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 2041
SOFTWARE: FastSEQ for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT .
ORGANISM: Homo sapiens
-US02-09671-1149
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LENGTH: 1461
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                                                                                                                        QKGSFQMVHCNCSVHECCECLVPVPTAK--
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                                                                                       VIGQDVVLPCVASG-
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                  EISDVTEDD - - AGTYFCIADNGNETIEAQA
                                                   QPINMVKPDPPLGLHMEITDDGNLKISWSSPPLVPFPLQYQVKYSENSTTV-IREADKIV
                                                                                                                                                                                             ANWNIQCWLKGDLKLFICYVESLFKNLFRNYNYKVHLLYVL-PEVLED-----
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llarity 19.6%;
Conservative 151
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                  ELTVQAQPEFLKQPTNIYAHESMDIV
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PCT-US02-09671-1150
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GENERAL INFORMATION:
APPLICANT: Zycos Inc.
TITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE REFERENCE: 08191-026WO1
PRIOR
PRIOR
                                                                CURRENT APPLICATION NUMBER: PCT/US02, CURRENT FILING DATE: 2002-03-28 PRIOR APPLICATION NUMBER: 60/279,495 PRIOR FILING DATE: 2001-03-28 PRIOR APPLICATION NUMBER: 60/292,544
                                  PRIOR
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 FILING DATE: 2001-05-21
APPLICATION NUMBER: 60/310,801
TTTNC DATE: 2001-08-08
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60/326,370
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1150

LENGTH: 1461

TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-09671-1150
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PRIOR APPLICATION NUMBER: 60/:
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                    VQ---SLSAYPLNSSCVIVSWILSPSD-------YKLMYFI--
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                                                                                                 NGTWSEDVGNHTKFTFL-----WTEQAHTVTVLAINSIGASVANENL-TFSWPMSKVNI
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Sequence 2, Application US/09853180; GENERAL INFORMATION:
APPLICANT: Chirica, Madaline
APPLICANT: Parham, Christi L.
APPLICANT: Kastelein, Robert A.
APPLICANT: Moore, Kevin W.
TITLE OF INVENTION: Mammalian Receptor Printer Reference: DX01074
CURRENT APPLICATION NUMBER: US/09/853,180
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,426
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 629
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                                                                                                                                                                                                                                                                                             IYFPPKILTSVGSNVSFHCIYKKENKIVPSKEIVWWMNLAEKIPQSQYDVVSDHVSKVTF 393
PVFPENNLQFQIRYGLSGKEVQWKMYEVYDA
                                                                                                                                                 TCRWSTSTIQSLAESTLQLRYHRSSLYCSDI
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                                                                         LSG---YTMWIRINHSLGSLDSPPTCVLPDS
                                                                                                               TCTWNAXKLTYI - - - -
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                                     LQGGKKYLVWVQAANALGMEESKQLQIHLDD
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                                  IVIPSAAVISRAE-TINATVPKTIIYWDS 244
                                                                                                               KSLE--TEEEQQYLTS----SYINISTDS 185
                                                                                                                                              PSIHPISEPKDCYLQSDGFYECIFQPIFL 505
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 K----SKSVSLPVPDLCAVYAVQVRCKRL 616
                                                                                                                                                                                       ICGKDISSGYPPDIPDEVTCVIYEYSGNM 142
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                                                                        VKPLPPSSVKAEITINIGLLK--ISWEK 560
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EGOD WATORDS	
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956 SDQFNSVNFSE 966	Qy
572TMLLENDSPSETIPEQTLLPDEFVSCLGIVNEELPSINTYFPQNIL	Db
903 TASVTCGPLLLEPETISEDISVDTSWKNKDEMMPTTVVSLLSTTDLEKGSVCI	Qy
532 FSVSSVNSLSNTIFLGELSLILNQGECSSPDIQNSVEEET	윧
843 YVIVPVIISSSILLLGTLLISHQRMKKLFWEDVPNPKNCSWAQGLNFQKPETFEHLFIKH	Qy
506 SLTL	ď
785 WLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDAGL	Qγ .
446 KPTDYKKENTGPLETRDYPQNSLFDNTTVVYIPDLNTGYKPQISNFLPEGSHLSNNNEIT	Db .
761 SPSDYK	Ψ
386 RRILLLIPKWLYEDIPNMKNSNVVKMLQENSELMNNNSSEQVLYVDPMITEIKEIFIPEH 445	뮹
732SWPMSKVNIVQSLSAYPLNSSCVIVSWIL 760	Qγ
339 ASISTGHLTSDNRGDIGLLLGMIVFAVMLSILSLIGIFNRSFRTGIK 385	Db
677 QRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSIGASVANFNLTF	, YQ
299 TGKRYWQPWSSPFFHKTPETVPQVTSKAFQHDTWNSGLTV	Db C
617 DGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNVTLLWKPLMKNDSLCSV	Oy .
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Search completed: May 18, 2002, 07:00:08 Job time: 577 sec

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TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids

TYPE: amino TOPOLOGY: us

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CURRENT APPLICATION DATA: CURRENT APPLICATION NUMBER: US/08/59,455B FILING DATE: 22-JAN-1996 PRIOR APPLICATION NUMBER: 08/58,153 FILING DATE: 28-DEC-1995 APPLICATION NUMBER: 08/570,142 FILING DATE: 11-DEC-1995 APPLICATION NUMBER: 08/569,485 FILING DATE: 11-DEC-1995 APPLICATION NUMBER: 08/566,622 FILING DATE: 08-DEC-1995 APPLICATION NUMBER: 08/566,622 FILING DATE: 04-DEC-1995 APPLICATION NUMBER: 08/562,663 FILING DATE: 27-NOV-1995 APPLICATION NUMBER: 08/562,663 FILING DATE: 27-NOV-1995 ATTORNEY/AGENT INFORMATION: NAME: Meiklejohn, Ph.D., Anita L. REGISTRATION NUMBER: 07334/017001 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEPHONE: 617-542-8906	RESULT 1 US-08-599-455B-4 Sequence 4, Application US/08599455B Patent No. 5972621 Patent No. 5972621 GENERAL INFORMATION: APPLICANT: Tartaglia, Louis A. APPLICANT: Tepper, Robert I. APPLICANT: Culpepper, Janice A. FITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS FITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OR NUMBER OF SEQUENCES: 44 CORRESPONDENCE ADDRESS: ADDRESSE: Fish & Richardson, P.C. STREET: 225 Franklin Street CITY: Boston STATE: MA COUNTRY: US COUNTRY: US ZIP: 02110-2804 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: Windows95	28 3785 60.5 894 2 US-08-599-455B-2 29 3785 60.5 894 4 US-09-069-781B-2 30 3779 60.4 895 4 US-08-827-962-19 31 3753 60.0 895 4 US-08-827-962-21 32 3057 48.9 569 1 US-08-306-231-3 421 6.7 77 4 US-08-803-346-64 34 395 6.3 76 4 US-08-803-346-63 37 345.5 5.5 918 2 US-08-803-346-63 38 316 5.1 708 1 US-08-825-558-6 40 316 5.1 708 1 US-08-825-558-2 41 316 5.1 708 2 US-09-058-263-2 42 316 5.1 708 2 US-09-058-263-2 43 316 5.1 708 3 US-09-058-263-2 44 313 5.0 837 1 US-07-923-976-2 45 309.5 4.9 75 4 US-08-803-346-60
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CORRENT APPLICATION NUMBER: US/09/069,781B
FILING DATE: 29-APRIL-1998
PRIOR APPLICATION NUMBER: US 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: US 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: US 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: US 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: US 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: US 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: US 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: US 08/569,485
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/569,485
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/562,663
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APPLICATION NUMBER: US 08/562,663
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: US 08/562,663
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/562,663
FILING DATE: 27-NOW-1995
APPLICATION NUMBER: US 08/562,663
FILING DATE: 27-DOCKET NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/082001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
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STREET: 225 Franklin Street
CITY: Boston
STATE: MA
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INCLUDING OBESIT
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GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA
                                                              GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED
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Sequence 1, Application US/09093814; Patent No. 6270981; GENERAL INFORMATION:
APPLICANT: Carpenter et al.
TITLE OF INVENTION: ASSAY SYSTEMS FOR L
FILE REFERENCE: REG 580-A; CURRENT APPLICATION NUMBER: US/09/093,81; CURRENT FILING DATE: 1998-06-09; PRIOR APPLICATION NUMBER: 60/049,108; PRIOR FILING DATE: 1997-06-09; NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSEQ for Windows Version 3
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LENGTH: 1165
TYPE: PRT
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bal Similarity 99.9%;
1164; Conservative
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Requence 11, Application US/08618957A

Patent No. 6355237

GENERAL INFORMATION:
APPLICANT: Snodgrass, H. Ralph
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas Joel
APPLICANT: Shafer, Alan Wayne
TITLE OF INVENTION: METHODS FOR USING TH
TITLE OF INVENTION: GENE AND ITS GENE PR
TITLE OF INVENTION: DEVELOPMENT
NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 AV
CITY: New York
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                     KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMMPTTVVSLLSTTDLEKGSVCISDQFN
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
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Best Local Similarity 99.9%;
Matches 1164; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POISSant, Brian M.
REGISTRATION NUMBER: 28,462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compati
OPERATING SYSTEM: DOS
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                                   VIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
                                                                                                                               REFNLNETKPRGKFTYDAVYCCNEHECHH 420
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RYGLSGKEVQWKMYEVYDAKSKSVSLPV
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GENERAL INFORMATION:
      ADDRESSEE: Pennie & Edmonds LLP STREET; 1155 Avenue of the America: CITY: New York
STATE: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,389A
FILING DATE: 29-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                             APPLICANT: Zupancic, Thomas APPLICANT: Shafer, Alan W. TITLE OF INVENTION: DETECTION RECEPTOR TITLE OF INVENTION: REGULAT NUMBER OF SEQUENCES: 16
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APPLICANT:
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Cloffi, Joseph
INFORMATION:
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Best Local Similarity 99.1%;
Matches 1155; Conservative
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
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REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-9741/886
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APPLICANT: Shafer, Alan Wayne
TITLE OF INVENTION: METHODS FOR USING TH
TITLE OF INVENTION: GENE AND ITS GENE PR
TITLE OF INVENTION: DEVELOPMENT
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of The Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,957A
FILING DATE: 20-MAR-1996
CLASSIFICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 958 amino acids
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                                                               ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 00
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; STRANDEDNESS: single
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; MOLECULE TYPE: protein
US-08-618-957A-8
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les 901; Conserv
                                       GLYVIVPVIISSSILLLGTLLISHQRMKKLFW GLYVIVPVIISSSILLLGTLLISHQRMKKLFW
                                                                                             GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLY
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                    TFEHLFIKHT-ASVTCGP--
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                                       EDVPNPKNCSWAQGLNFQK-----PE 893
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/355,888A
FILING DATE: 14-DEC-1994
CLASSIFTCATTON: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7225-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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                                  FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPPFQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFRSPLMSVQPINMVKPDPP
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ÆNTION: Hu-B1.219,
ÆNTION: RECEPTOR
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Cioffi, Jos
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94.18;
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RESULT 8
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Patent No. 5869610
GENERAL INFORMATION:
                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: FastSEQ for Windows Versic

CURRENT APPLICATION DATA:

CURRENT APPLICATION NUMBER: US/08/693,697
ATTORNEY/
NAME:
                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                       NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRE
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                   CLASSIFICATION:
                               FILING DATE:
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ET: 1155 Avenue o
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10036-2711
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Cioffi, Jo
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Shafer, Alan
INFORMATION:
ant, Brian M.
                                                                                                                                                                        ADDRESS:
                             05-AUG-1996
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REFERENCE/DOCKET NUMBER: 8907
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IS-08-693-697-8
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                                                                       TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
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94.1%;
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Pred. No. 0;
7; Mismatches
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NAME: POISSANT, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-640-389A-3
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GENERAL INFORMATION:
APPLICANT: Snodgrass
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Best Local Similarity
Matches 901; Conserv
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,389A
FILING DATE: 29-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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STREET: 1155 Aven
CITY: New York
STATE: New York
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                                                                                NGHYETAVEPKENSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
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94.18;
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RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
REGULATING REPRODUCTIVE BIOLOGY
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RESULT 10
US-08-693-696-8
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                                                       APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE F
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                                  ESSEE: Pennie & ET: 1155 Avenue : New York
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 amino acids
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Best Local Similarity 94.1%;
Matches 901; Conservative
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                          FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP 240
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TOPOLOGY: 1ii
; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-693-697-33
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US-08-693-697-33
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INFORMATION FOR SEQ ID NO: 33
SEQUENCE CHARACTERISTICS:
LENGTH: 908 amino acids
TYPE: amino acid
Query
Best L
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSEQ for Windows Ver.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219,
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/693,697
FILING DATE: 05-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                        NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0037-999
RELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEPHONE: 650-493-5556
y Match
Local
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CITY: Ne
STATE: N
COUNTRY:
                                                                                                        TYPE: amino a
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New York
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5869610
Similarity
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Cioffi, Joseph
Zupancic, Thomas J.
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77.0%;
99.1%;
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4816;
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RESULT 12
US-08-588-190-3
; Sequence 3, Application U
; Patent No. 5856098
; GENERAL INFORMATION:

US/08588190

APPLICANT:
APPLICANT:
APPLICANT:

TT: Snodgrass, H. ReTT: Cioffi, Joseph
TT: Cioffi, Joseph
TT: Zupancic, Thoma:
TT: Shafer, Alan Wa:
TNVENTION: DETECT:

Thomas Joel

Ralph

Alan Wayne DETECTION

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APPLICANT: TITLE OF I

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                         PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV
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GLYVIVPVIISSSILLLGTLLISHQRMKKLFW
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                                                     CVIVSWILSPSDYKLMYFIIEWKNLNED
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       EDVPNPKNCSWAQGLNFQK--PETFEHL
EDVPNPKNCSWAQGLNFQKKMPGTKELL
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FILING DATE: 18-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POISSANT, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 008907-0029
REFERENCE/DOCKET NUMBER: 008907-0029
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 65141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
ILENGTH: 960 Amino Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Vers
CURRENT APPLICATION DATA:
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CITY: 1
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Pred. No. 0;
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                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Versic
CURRENT APPLICATION DATA:
                                                                          APPLICATION NUMBER: US
FILING DATE: 20-MAR-1S
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                  TITLE OF
TELECOMMUNICATION INFORMATION: TELEPHONE: 650-493-4935
                                                   ATTORNEY/AGENT INFORMATION NAME: Poissant, Brian M
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CORRESPONDENCE ADDRESS:
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ZIP: 10036-2811
                       NAME: Poissant, Brian M. REGISTRATION NUMBER: 28,462 REFERENCE/DOCKET NUMBER: 00
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20-MAR-1996
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Best Loc
Matches
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
S-08-618-957A-3
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93.9%;
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Pred. No. 0;
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US-08-618-957A-10
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ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,
FILING DATE: 20-MAR-1996
CLASSIFICATION AARA-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 435
PRIOR APPLICATION NUMBER: FILING DATE:
APPLICATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 0089
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-4935
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 896 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOCOLOGY: 1inear
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Patent No.
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Best Local Similarity
Matches 888; Conserv
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APPLICANT: Shafer, Alan Wayne
TITLE OF INVENTION: METHODS FOR USIN
TITLE OF INVENTION: GENE AND ITS GEN
TITLE OF INVENTION: DEVELOPMENT
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
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CITY: New York
STATE: NY
COUNTRY: USA
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GLYVIVPVIISSSILLLGTLLISHQRMKKLF
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GENERAL INFORMATION:
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APPLICANT: Cioffi, Joseph
APPLICANT: Cupancic, Thom
APPLICANT: Shafer, Alan W
TITLE OF INVENTION: Hu-B1
TITLE OF INVENTION: RECEP
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                        ADDRESSEE: Pennie & E
STREET: 1155 Avenue o
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
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5869610
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Cioffi, Joseph
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Hu-B1.219,
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TYPE: amino acid

STRANDEDNESS: sing

TOPOLOGY: linear

MOLECULE TYPE: prote

FRAGMENT TYPE: inter

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Best Local Similarity 99.7%;
Matches 888; Conservative
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                                                             PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWI
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                                      SSVKAEITINIGLLKISWEKPVFPENNLQFQIR
                                                                                             PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVV
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linear
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MDIKVPMRGPEFWRIINGDTMKKEKNV
                              YGLSGKEVQWKMYEVYDAKSKSVSLPV
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842	783 GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 842	dd
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782	723 GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 782	DD.
780	721 GASVANPNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780	Qy
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Search completed: May 18, 2002, 06:53:57 Job time: 5722 sec

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nypornetical prote cysteine synthase/		E97175	21	309	0.6	7	75.4
hetical		2062) N	S CO		ı ~	L
phoserine		136	N	v	٠	7	72
Ξ		63	N	့မ		7	71
nserved hypoth		E90186	Ŋ	293	0.6	7	70
etylneuramin		405	Ŋ	9		7	
osphodiestera		ВРТ	ட	ø	•	7	86
tein		S65961	N	σ.		7	
_		469	N	œ		7	
tical prot		222	N	~I ·		7	
nknown protein,		ტ სე	N	ч		7	
pistil extensin-li		047	N	σ,		7	ω :
onine am		541	N	UI.		7	
ypothetical pr		T32939	N	S (7.	
ble membrane	_	901	S) I	J (7	
hetical prot		156	N	O I		7	9
F52E		913	N	UT.		7	
ble	-	071	N	S.		7	
robable		147	N	4		7	
nserved		173	N	4		7	
amic		342	N	4		7	4
ical		338	N	ω		7	
etical pro	-	892	N	ω		7	2
transpo		120	N	w	•	7	ĭ
ridylate		223	N	w		7	ŏ
e membran		979	Ь	w		7	9
lloproteinase		3599	ш	N		7	<u>~</u>
pothetical		7554	N	ь,		7	17
thetical		w	N	_	•	7	50
ypothetical p		7102	<u> </u>	Φ		7	5
in typ		w.	N	യ	•	7	4
teine syntha		4186	N	190	•	7	ω
7-2 fimbrial pr	-	OECF	_	Ф	•	7	2
lin type F7-1 p		C43597	N	187	•	7	i i
imbrial pr		OECK	ட	œ	•	7	ō
mbrial protein		40ECP	Н	œ	٠	7	õ
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bosomal protei		5BSL	<u>, , , , , , , , , , , , , , , , , , , </u>	146	٠	7	ភ
netical		093	N	144	٠	7	¥
othetical p		8288	N		٠	7	ຜ
e memb		7051	Ŋ	w	٠	7	ວັ
tical prot	•	136	N	127		7	ĭ
hypothetical prote		44	ผ	127	•	7	õ
	_ •						

ALIGNMENTS

RESULT 1

\$68441

leptin receptor, splice form Ob-Re - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-2000 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
C;Accession: \$68441
R;Lee, G:H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;
Rature 379, 632-635, 1996
A;Title: Abnormal splicing of the leptin receptor in diabetic mice.
A;Reference number: \$68437; MUID:96231997
A;Accession: \$68441
A;Reference number: \$68437; MUID:96231997
A;Accession: \$68441
A;Residues: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-805 <LIEE>
A;Cross-references: EMBL:U49110; NID:g1195492; PIDN:AAC52424.1; PID:g1195493
A;Experimental source: splice form Re; tissue hypothalamus
A;Mote: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C;Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:
C;Genetics:
A;Gene: Ob-Re
C;Keywords: alternative splicing; appetite.

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A; Reference number: $68437; MUID: 96231997
A; Accession: $68437
A; Status: nucleic acid sequence not shown; transl
A; Molecule type: mRNA
A; Residues: 1-894 < LEE>
A; Cross-references: EMBL: U49106; NID: g1195484; PI
A; Experimental source: splice form Ra; tissue hyp
A; Note: the nucleotide sequence was submitted to
C; Comment: For alternative splice forms, see PIR:
C; Genetics:
A; Gene: Ob-Ra
C; Keywords: alternative splicing; appetite
                                                                                                                                                                                                A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-796, 'GMCTVLFMD' <LEE2>
A; Cross-references: EMBL:U49110; NID:g1195492; PIDN:AAC5242
A; Experimental source: splice form Re; tissue hypothalamus
A; Note: the nucleotide sequence was submitted to the EMBL I
A; Note: this sequence from splice form Re is included to p:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-2000 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
C;Accession: S68439; S68441
R;Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; I Nature 379, 632-635, 1996
A;Title: Abnormal splicing of the leptin receptor in diabetic mice.
A;Reference number: S68437; MUID:96231997
A;Accession: S68439
A;Status: nucleic acid sequence not shown; translation not shown
A;Residues: 664-892 <LEE1>
A;Residues: 664-892 <LEE1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:U49108; NID:g1195488; A;Experimental source: splice form RC; tissue h A;Note: the nucleotide sequence was submitted t A;Accession: $68441
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Best Local S
Matches 42
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les: Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alternative splicing;
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42; Conser
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larity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                        (house mouse)
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                                                                                                                                                                                                                                                                 Montez, J.M.; Carroll,
                                                                                                                                                                                                            of the leptin MUID:96231997
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                          mouse
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                                                                                                                                                                                                                               receptor
                                                                                                                                                                          translation
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                                                                e hypothalamus
ed to the EMBL D
PIR:S68437, PI
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2.9e-35;
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to the EMBL
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                                                                                                                    PIDN: AAC52420.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIDN: AAC52422.1; PID: g1195489
                                                                                                                                                                                                                                                                K.M.; Darvishzadeh,
                                                                                                                                                                                                                                                                                                    #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 892;
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                                                                 L Data Library, February PIR:S68438, PIR:S68439,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Data Library,
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                                                                                                                    PID:g1195485
                                                                                                                                                                                                                                                                                                      31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete sequence
8, PIR:S68439, PIR
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                                                                                                                                                                                                                                                                   Lee,
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                                                                1996
PIR:S6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR:S6
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                          A; Note: this sequence from C; Comment: For alternative C; Genetics:
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C;Species: Mus musculus (nouse mour, C;Date: 17-Jul-1998 #sequence_revision 17. C;Accession: $68440

R;Lee, G.H.; Proenca, R.; Montez, J.M.; C;
Nature 379, 632-635, 1996

A;Title: Abnormal splicing of the leptin A;Reference number: $68437; MUID:96231997
                                                                                                                                     A;Cross-references: EMBL:U49109; NID:g1195
A;Experimental source: tissue hypothalamus
A;Note: the nucleotide sequence was submit
C;Comment: For alternative splice forms, s
C;Genetics:
A;Gene: Ob-Rd
C;Keywords: alternative splicing; appetite
F;840-860/Domain: transmembrane #status pr
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
S68440
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                                                                                                                                                                                                                                                           A;Status: nucleic acid sequence
A;Molecule type: mRNA
A;Residues: 1-900 <LEE>
   당
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Best Local
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Best Local
                               500
                                                                                                                                                                                                                                                                                                                                                                                                                              receptor,
FQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPPS 541
                                                             . Similarity 42; Conser
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                                                         conservative
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                                                                                                                                                                                                                                                                                            not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                           Score 42
Pred. N
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                                                             Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misma
                                                                           2; DB 2; L
No. 2.9e-35;
                                                                                                                                        e; transmembrane protein redicted <TMM>
                                                                                                                                                                                                 tted to the EMBL Data Library, February see PIR:S68437, PIR:S68438, PIR:S68439,
                                                                                                                                                                                                                                                                                                                                       receptor in diabetic mice.
                                                                                                                                                                                                                                                                                                                                                                   arroll, K.M.; Darvishzadeh,
                                                                                                                                                                                                                                                                                                                                                                                                 -Jul-1998 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDSVVKPLPPS 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; DB 2; Length 894;
No. 2.9e-35;
                                                              atches
                                                                                                                                                                                                                                              5490; PIDN:AAC52423.1; PID:g1195491
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                                                                                                                                                                                                                                                                                           translation not shown
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                                                                                        Length 900;
                                                              Indels
                                                             0;
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                                                             Gaps
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                                                              <u>.</u>
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PIR:
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A; Molecule type: mRNA
A; Residues: 664-1162 <LEE1>
A; Cross-references: EMBL:U49107; NID:g119548
A; Experimental source: splice form Rb; tissu
A; Note: the nucleotide sequence was submitte
A; Note: only a part of the translation is sh
A; Accession: S68441
A; Status: nucleic acid sequence not shown; the status: nucleic acid sequence not shown; the status: nucleic acid sequence not shown; the status: nucleic acid sequence not shown; the status: nucleic acid sequence not shown; the status is nucleic acid sequence not shown; the status is nucleic acid sequence not shown; the status is nucleic acid sequence not shown; the status is nucleic acid sequence not shown; the status is nucleic acid sequence not shown; the status is not shown; the status is nucleic acid sequence not shown; the status is not shown; the stat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Mus musculus (house mouse)
C; Date: 17-Jul-1998 #sequence_revision 31
C; Accession: $68438; $68441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
S68438
                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-796, 'GMCTVLFMD' <LEE2>
                                                                                                                          A; Experimental source: splice form Re; ti
A; Note: the nucleotide sequence was submi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Lee, G.H.; Proenca, R.;
Nature 379, 632-635, 1996
                                                                                                                                                                                                                                                    A;Cross-references: EMBL:U49110; NID:g119!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leptin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor, splice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  form Ob-Rb -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5486; PIDN:AAC52421.1; PID:g1195487 ssue hypothalamus tted to the EMBL Data Library, Febr
ssue hypothalamus
tted to the EMBL Data Library, February 1996
is included to produce a complete sequence
see PIR:S68437, PIR:S68438, PIR:S68439, PIR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor in diabetic mice
                                                                                                                                                                                                                                                    5492; PIDN:AAC52424.1; PID:g1195493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -Dec-2000 #text_change 31-Dec-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                        translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         February 1996
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alternative

splicing;

appetite

splice

form Re

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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-889, 'RADTL' <TA2>
A;Cross-references: DDBJ:D85557
A;Accession: JC4897
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-796, 'G', 1157-1158, 'TVLLLN' <7
A;Cross-references: DDBJ:D85559
RESULT 7
S74225
leptin rece
C; Species:
                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-889, 'RADTL' <II2>
A; Cross-references: DDBJ: D84125; NID: g1374707; PIDN: BAA122
A; Experimental source: adipose cell
C; Comment: This receptor is obese-phenotype-linked mutant,
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leptin receptor, Ob-Rb - rat C; Species: Rattus norvegicus (Norway rat) C; Species: Rattus norvegicus (Norway rat) C; Date: 15-Aug-1996 #sequence_revision 13-Mar-1997 #text_change C; Accession: JC4895; JC4896; JC4897; PC4184; JC4797 R; Takaya, K.; Ogawa, Y.; Isse, N.; Okazaki, T.; Satoh, N.; Masuz Biochem. Biophys. Res. Commun. 225, 75-83, 1996 A; Title: Molecular cloning of rat leptin receptor isoform comple A; Reference number: JC4895; MUID: 96332408 A; Accession: JC4895
                                                                                                                                                                                                                                          A;Gene: fa
C;Keywords: appetite; transmembrane protein
F;840-860/Domain: transmembrane #status predicted <TMM>
F;861-1162/Domain: intracellular #status predicted <INT>
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R;Iida, M.; Murakami, T.; Ishida, K.; Mizuno, A.;
Biochem. Biophys. Res. Commun. 222, 19-26, 1996
A;Title: Phenotype-linked amino acid alteration ir
A;Reference number: JC4797; MUID:96212906
A;Accession: JC4797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Iida, M.; Murakami, T.; Ishida, K.; Mizuno, A.; Kuwaj Biochem. Biophys. Res. Commun. 224, 597-604, 1996
A; Title: Substitution at codon 269 (glutamine-proline)
A; Reference number: PC4184; MUID:96295531
A; Accession: PC4184
A; Molecule type: mRNA
A; Residues: 840-1162 < IID>
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A;Molecule type: mRNA
A;Residues: 1-1162 <TAK>
A;Cross-references: DDBJ:D85558;
A;Accession: JC4896
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Best Local Similarity 100.0%;
Matches 42; Conservative (
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C;Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 05-Nov-1999
C;Accession: S74225
R;Wang, M.Y.; Zhou, Y.T.; Newgard, C.B.; Unger, R.H.
FEBS Lett. 392, 87-90, 1996
A;Title: A novel leptin receptor isoform in rat.
A;Reference number: S74225; MUID:96368027
A;Accession: S74225
A;Molecule type: mRNA
A;Residues: 1-895 <WAN>
A;Cross-references: EMBL:U53144; NID:g1395212; PIDN:AAB03088.1; PID:g1395213
A;Experimental source: strain Sprague-Dawley; tissue type brain
C;Genetics:
A;Gene: rOb-R
C;Keywords: appetite; transmembrane protein
F;840-860/Domain: transmembrane #status predicted <TMM>
                                                                                hypothetical protein CAC1767 [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C; Accession: B97118

R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; I R; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A; Reference number: A96900; MUID:21359325; PMID:21359325

A; Accession: B97118

A; Status: preliminary

A:Molecule ture: Num
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A;Reference number: Z21774
A;Accession: T38142
A;Accession: T38142
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-124 <PEA>
A;Residues: 1-124 <PEA>
A;Cross-references: EMBL:Z99295; PIDN:CAB16572.1; GSPDB:GN00066; SPDB:SPAC22A12.02c
A;Experimental source: strain 972h-; cosmid c22A12
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C;Date: 03-Dec-1999 #sequence_revision: C;Accession: T38142
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C; Superfamily:
                       A; Cross-references: GB: AE001437;
                                          A; Molecule type: DNA
A; Residues: 1-222 <KUR>
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PIDN:AAK79733.1; PID:g15024737; GSPDB:GN00168 um acetobutylicum ATCC824
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source:

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probable DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) - Sulfolobus solf N;Alternate names: endonuclease III; protein c04006
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 20-Jun-2000
C;Accession: S75373
R;Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penn A;Col. Microbiol. 22, 175-191, 1996
A;Title: Organizational characteristics and information content of an archaeal gence A;Reference number: S73076; MUJD:97055432
A;Accession: S75373
A;Status: nucleic acid sequence not shown; translation not shown
A;Residues: 1-236 <SEN>
A;Cross-references: EMBL:Y08257; NID:g1707772; PID:g1707778
A;Experimental source: strain P2
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1 C;Superfamily: apurinic/apyrimidinic endonuclease III
C;Superfamily: apurinic/apyrimidinic endonuclease III
C;Keywords: 4Fe-4S; carbon-oxygen lyase; metalloprotein
F;204,211,214,219/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
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A;Residues: 1-425 <STO>
A;Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06445.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
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A;Gene: CAC1767
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hypothetical protein UL27 - human cytomes
C;Species: human cytomegalovirus, human l
A;Note: host Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07
C;Accession: S09790
R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bo
M.; Barrell, B.G.
Curr. Top. Microbiol. Immunol. 154, 125-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein PA0344 [imported] - Ps C; Species: Pseudomonas aeruginosa C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #sequence_revision 15-Sep C; Accession: F83602
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Miadman, S.; Yuan, Y.; Brody, L.L.; Coulter, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudo A; Reference number: A82950; MUID: 20437337, A; Accession: F83602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: The complete sequence and gene organization of the short unique region of he A;Reference number: JQ2346; MUID:94014999 ,
A;Reference number: JQ2353
A;Rocession: JQ2353
A;Rolecule type: DNA
A;Residues: 1-498 <ZEL>
C;Keywords: glycoprotein; transmembrane protein
F;1-18/Domain: signal sequence #status predicted <MAT>
F;19-498/Product: glycoprotein E #status predicted <MAT>
F;396-412/Domain: transmembrane #status predicted <TMM>
F;444,60,133,148,370/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                       RESULT
S09790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glycoprotein E precursor - turkey herpesvi N; Alternate names: ORF 8 protein C; Species: turkey herpesvirus C; Date: 30-Sep-1993 #sequence_revision 20-C; Accession: JQ2353 C; Accession: JQ2353 R; Zelnik, V.; Darteil, R.; Audonnet, J.C.; J. Gen. Virol. 74, 2151-2162, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
F83602
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C; Superfamily:
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A;Residues: 1-459 <STO>
A;Cross-references: GB:AE004472; GB:AE004091; NID:g9946188; PIDN:AAG03733.1; GSPDB:GN
A;Experimental source: strain PAO1
C;Genetics:
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8; Conservative
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8; Conservative
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50; MUID:20437337
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human herpesvirus 5
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NO. 17;
natches
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, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -Sep-2000 #text_change 31-Dec-2000
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                                                 ni, R.; Brown, C.M.; Cerny, R.; Horsnell, T
                                                                                            -Sep-1990 #text_change 08-Oct-1999
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125-169, 1990

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hypothetical protein T1E3.140 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 *sequence_revision 20-Apr-2000 *text_change 20-Accession: T48474 R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R. ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X. submitted to the Protein Sequence Database, April 2000 A;Reference number: Z24491 A;Accession: T48474 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-864 <BEV> A;Cross-references: EMBL:AL162972 A;Experimental source: cultivar Columbia; BAC clone T1E3 C;Genetics:
                                                                              R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.;
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; V
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
A; Accession: G87640
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-937 <STO>
A; Cross-references: GB:AE005673; NID:g13424831; PIDN:AAK25123.1
C; Genetics:
A; Gene: CC3161
                                                                                                                                                                                                                                                                                                                                                                                     RESULT
G87640
                                                                                                                                                                                                                                                                                                           TonB-dependent receptor [imported] - Caulobacter crescentus C; Species: Caulobacter crescentus C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change C; Accession: G87640
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A; Molecule type: DNA
A; Residues: 1-608 < CHE>
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A; Accession: S09790
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A; Introns: 612/2;
A; Note: T1E3.140
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8; Conserv
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ilarity 100.0%;
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              0.7%;
                                                                                                                    NID:g13424831; PIDN:AAK25123.1; GSPDB:GN00148
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Nelson, K.E.; Eisen, J.; Heidelberg, J.

Nelson, K.E.; Haft, D.H.; Kolor

T. Fraser, C.M.
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          hypothetical protein F22E1
C; Species: Caenorhabditis
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hypothetical protein F22E10.4 - Cae C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revis C; Accession: T21269 R; Gardner, A. submitted to the EMBL Data Library, A; Reference number: Z19398
                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-1291 <WIL>
A; Cross-references: EMBL: Z67882; PIDN: CAA91
A; Experimental source: clone F22E10
C; Genetics:
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A; Introns: 69/2; 120/2; 162/3; 207/2;
C; Superfamily: unassigned ATP-binding
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A; Molecule type: DNA
A; Residues: 1-1270 <WIL>
A; Cross-references: EMBL: Z67882; PIDN: CAA91
A; Experimental source: clone F22E10
C; Genetics:
A; Gene: CESP: F22E10.4
                                                                                                                                                     A; Map position: X A; Introns: 19/3; 63/2; 81/3; 114/2; 156/3; 201/2; 258/3; 354/1; 642/2; 724/1; 791/3; C; Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog
                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: T21267
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                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F22E10.2 - Caenorhabdi
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-C; Accession: T21267
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Similarity 100.0%;
8; Conservative
                                                                 0.7%;
Similarity 100.0%;
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. 42;
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Caenorhabd

itis elegans

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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change i8-Feb-ZUUU C;Accession: T21266

R;Gardner, A.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z19398
A;Accession: T21266
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1318 <WIL>
A;Residues: 1-1318 <WIL>
A;Cross references: EMBL: Z67882; PIDN:CAA91799.1; GSPDB:GN00028; CESP:F22E10.1
A;Experimental source: clone F22E10
C;Genetics:
A;Gene: CESP:F22E10.1
A;Map position: X
A;Introns: 26/3; 81/3; 114/2; 156/3; 201/2; 258/3; 300/2; 396/3; 676/2; 818/3; 939/3; 10
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F22E10.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #
C;Accession: T21268
R;Gardner, A.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z19398
A;Accession: T21268
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1327 <WIL>
A;Cross-references: EMBL: Z67882; PIDN: CAA91801.1; GS: A;Experimental source: clone F22E10
C;Genetics:
A;Gene: CESP: F22E10.3
                                                        hypothetical protein XF0098 [imported] - Xylella C; Species: Xylella fastidiosa C; Date: 18-Aug-2000 #sequence_revision 20-Aug-200 C; Accession: H82849 R; anonymous, The Xylella fastidiosa Consortium of Nature 406, 151-157, 2000 A; Title: The genome sequence of the plant pathoge A; Reference number: A82515; MUID: 20365717 A; Note: for a complete list of authors see refere A; Accession: H82849
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A; Introns: 23/3; 93/3; 213/2; 270/3; 686/2; 827/3; 1261/3
C; Superfamily: unassigned ATP-binding cassette proteins;
A; S'catus: preliminary
A; Molecule type: DNA
A; Residues; 1-64 <SIM
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Best Local
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8; Conser
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llarity 100.0%;
Conservative
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llarity 100.0%;
Conservative
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Pred. No
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Pred. No. 43;
0; Mismatches
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                                                                                                                       Xylella
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ribosomal protein L15 - Bacillus licheniforn
C; Species: Bacillus licheniformis
C; Date: 13-Jan-1995 #sequence_revision 13-Ja
C; Accession: S34404
R; Tschauder, S.; Driessen, A.J.M.; Freudl, F
Mol. Gen. Genet. 235, 147-152, 1992
A; Title: Cloning and molecular characterizat
A; Reference number: S30115; MUID:93062802
A; Accession: S34404
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A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A
as-Neto, E.; Docena, C.; El-Dorry, H.; Facin
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajim
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliv
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr.
A;Authors: da Silva, A.C.R.; da Silva, F.R.;
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M
A;Reference number: A59328
A;Genetics:
annotation
                                                        R;Ito, T.; Katayama, Y.; Hiramatsu, K. Antimicrob. Agents Chemother. 43, 1449-149. A;Title: Cloning and nucleotide sequence of A;Reference number: Z22733; MUID:99278010. A;Accession: T44104. A;Status: preliminary; translated from GB,
                                                                                                                                                                                      hypothetical protein [imported] - Staphyloc; Species: Staphylococcus aureus C; Date: 21-Jan-2000 #sequence_revision 21 C; Accession: T44104
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A; Residues: 1-72 <TSC>
A; Cross-references: EMBL: X70087
C; Genetics:
A; Gene: rpl15
C; Superfamily: Escherichia coli ribosomal
C; Keywords: protein biosynthesis; ribosome
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S34404
A; Molecule type: DNA
A; Residues: 1-87 <ITO
A; Cross-references: 1
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 EMBL: D86934;
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 PIDN:BAA
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1449-1458, 1999
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tajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
a Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
ys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
                                                                                                                              determination of the entire mec DNA of pre-m
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latches
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matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   zation of the secY genes from Bacillus liche
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 32206.1
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C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change.2
C;Accession: AD1704
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, E.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, C.; A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1704
                                                                                                                                                                                                                                                                                                                                    Class I heat-shock protein (chaperonin) GroES [imported] - Listeria monocyto C; Species: Listeria monocytogenes
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C; Accession: AE1333
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.I.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitolok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AE1333
A; Control of the contr
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-94 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAD00147.1;
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: groES
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A;Molecule type: DNA
A;Residues: 1-94 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC97404.1;
A;Experimental source: strain Clip11262
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Similarity 100.0%;
7; Conservative
                             Similarity 7; Conserv
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                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         نَّهُ:; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.6%;
                                                  0.6%;
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Pred. No. 46;
0; Mismatches
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Pred. No
                                                    Score 7;
Pred. No.
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Mismatches
                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kurapkat, G.; Madueno, E.;
, A.; Vazquez-Boland, J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                      PID:g16411539; GSPDB:GN00177
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                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F:; Berche, P.; Entian, K.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 27-Nov-2001
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                             Gaps
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Voss, H.; W
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Voss, H.; Wehland
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Fsihi, H.
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                                                RESULT
AC1518
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C; Keywords:
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hypothetical protein C; Species: Listeria i
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Best Local
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RESULT 26
$59321
hypothetical protein L3125 (L3123 internal or C; Species: Saccharomyces cerevisiae C; Date: 29-Nov-1995 #sequence_revision 05-Sep C; Accession: $59321
R; Delius, H.
submitted to the EMBL Data Library, June 1995 A; Description: 36.8 kb of S.cerevisiae chromo A; Reference number: $59313
A; Accession: $59321
A; Status: conceptual translation of pseudoger
                                                                                                                                                                                                                  hypothetical protein lmo0675 [imported] - Lis C; Species: Listeria monocytogenes C; Date: 27-Nov-2001 #sequence_revision 27-Nov C; Accession: AC1159 R; Glaser, P.; Frangeul, L.; Buchrieser, C.; A.; Dominguez-Bernal, G.; Duchaud, E.; Durand, D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001 A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kuok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Fitle: Comparative genomics of Listeria spea; Reference number: AB1077; MUID:21537279; PM A; Accession: AC1159 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-104 <GLA> A; Experimental source: strain EGD-e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-101 <DEL>
A; Cross-references: EMBL:X91258; NID:g99568
A; Experimental source: strain S288C
C; Comment: There is no evidence that this s
C; Genetics:
                                                                                                                                                                                                   A; Experimental source: C; Genetics:
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Best Local Similarity
7; Conserve
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                                      859 TLLISHQ 865
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                                                                             Conservative
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53
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                                                                                                 100.0%;
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                                                                                                 Score 7;
Pred. No
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                                                                           DB 2;
lo. 51;
tches
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A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Listeria monocytogenes (strain EGD-e)
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                                                                                                                                                                                                                                              98753.1; PID:g16410064; GSPDB:GN00177
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PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              )6; PIDN:CAA62544.1; PID:g995695
                                                                                                                   Length 104;
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lin0683

[imported]

Listeria innocua (strain Clipl1262)

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AE1445

Appothetical protein lin0100 [imported] - Listeria innocua (strain Clip11262)

C; Species: Listeria innocua

C; Species: Listeria innocua

C; Species: Listeria innocua

C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001

C; Accession: AE1445

R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A; Aŭthors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitour ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.

A; Title: Comparative genomics of Listeria species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: AC2259
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC2259
A;Status: preliminary
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A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A; Title: Comparative genomics of Listeria species.

A; Reference number: AB1077; MUID:21537279; PMID:11679669

A; Accession: AC1518
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C;Accession: AC1518
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baguero,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-123 <KUR>
A; Cross-references: GB: BA000019; PIDN: BAB75325.1;
A; Experimental source: strain PCC 7120
C; Genetics:
A; Gene: all3626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein all3626 [imported] - Anabaena sp. (strain PCC 7120) C;Species: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-104 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC95915.1;
A;Experimental source: strain Clip11262
C;Genetics:
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Matches 7
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Best Local S
Matches 7
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7; Conserv
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d, L.; Dussurget, O.;
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; Entian, K.D.; Fsihi, H
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Voss, H.; W
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                                    urnam, A.; Ma
H.; Wehland,
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                                                                                                                               ; Bloecker
Fsihi, H.
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Wehland,
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probable membrane protein - Mycobacterium tuc; Species: Mycobacterium tuberculosis C; Species: 17-Jul-1998 #sequence_revision 17-Jul C; Accession: D70518
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garn; Connor, R.; Davies, R.; Devlin, K.; Feltwe, Rajandream, M.A.; Rogers, J.; Rutter, S.; Sellature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor A; Title: Deciphering the biology of Mycobacter, A; Reference number: A70500; MUID:98295987
A; Accession: D70518
A; Status: preliminary; nucleic acid sequence A; Molecule type: DNA
A; Residues: 1-134 < COL>
A; Cross-references: GB: Z97193; GB: AL123456; 14, Experimental source: Strain H37Rv
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein lmo2305 [imported] - Li
C; Species: Listeria monocytogenes
C; Date: 27-Nov-2001 #sequence_revision 27-No
C; Accession: AI1362
R; Glaser, P.; Frangeul, L.; Buchrieser, C.;
.; Dominguez-Bernal, G.; Duchaud, E.; Durand
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; K
ok, C.; Schlueter, T.; Simoes, N.; Tierrez,
A; Title: Comparative genomics of Listeria sp
A; Reference number: AB1077; MUID:21537279; P
A; Accession: AI1362
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-127 <GLA>
A; Cross-references: GB:NC_003210; PIDN:CAD00
A; Experimental source: Strain EGD-e
C; Genetics:
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A; Accession: AE1445
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-127 <GLA>
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Best Local Similarity
7; Conserv
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Pred
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z, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
species.
; PMID:11679669
                                                                                                                                                                                       lor, K.; Whitehead, S.; Barrell, B.G. acterium tuberculosis from the complete geno
                                                                                                                                                                                                                                                      arpier, T.; Churcher, C.; Harris, D.; Gordon
twell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Seeger, K.; Skelton, S.; Squares, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .; Amend, A.; Baquero, F.; Berche, P.; Bloec and, L.; Dussurget, O.; Entian, K.D.; Fsihi,
                                                                                                                                                                                                                                                                                                                                                       -Jul-1998 #text_change 02-Sep-2000
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5; NID:g3261816; PIDN:CAB10033.1; PID:e32486

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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987

A;Accession: C70937
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C; Date: 18-Aug-2000 #sequence_revision
C; Accession: C82889
R; Glass, J.I.; Lefkowitz, E.J.; Glass,
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C82889
hypothetical protein UU445 [imported] -
                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-144 <COL>
A; Cross-references: GB: AL021957; GB: AL123456;
A; Experimental source: strain H37Rv
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
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A; Residues: 1-141 <GLA>
A; Cross-references: GB: AE002141; GA; Experimental source: serovar 3;
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C; Superfamily:
                     Å0
                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein Rv2185c - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2 C;Accession: C70937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; submitted to GenBank, February 2000
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Best Local S
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                     969 GTEVTYE
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                                                        Conservative
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                                                                                                                                        coelicolor hypothetical
                                                                                                                                                                                                                                                           acid sequence not shown;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 7; DB 2
Pred. No. 64;
0; Mismatches
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                                                      Score 7; DB 2
Pred. No. 68;
0; Mismatches
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                                                                    DB 2;
. 68;
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. 67;
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RESULT 36
AH1193
hypothetical
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C;Superf
C;Keywor
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protein lmo0952 [imported]

Listeria monocytogenes (strain EGD-e)

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A; Residues: 1-140 CMAKS

A; Cross Teferences: DBD:DBD:D00619; NID:g216336; PIDN:BAA00494.1; PID:g216338

R; Suh, J.W.; Boylan, S.A.; Thomas, S.M.; Dolan, K.M.; Oliver, D.B.; Price, C.W.

Mol. Microbiol. 4, 305-314, 1990

A; Title: Isolation of a secty homologue from Bacillus subtilis: evidence for a common A; Reference number: S08628; MUID:90251170

A; A; A; Cross Teferences: S08628; MUID:90251170

A; Residues: 94-146 <SUHY
A; Residues: 94-146 <SUHY
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C; Date: 30-Jun-1992 #sequence_revision
C; Accession: S12682; JS0491; S08628; A
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J. Biochem. 107, 603-607, 1990
A; Title: Cloning and characterization of a
A; Reference number: JS0490; MUID:90292990
A; Accession: JS0491
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A;Residues: 1-146 <YOS>
A;Cross-references: EMBL:M31102; NID:g1184272; PIDN:AAB59117.1; PID:g143577
A;Cross-references: EMBL:M31102; NID:g1184272; PIDN:AAB59117.1; PID:g143577
A;Cross-references: EMBL:M31102; NID:g1184272; PIDN:AAB59117.1; PID:g143577
A;Cross-references: EMBL:M31102; NID:g1184272; PIDN:AAB59117.1; PID:g143577
A;Cross-references: EMBL:M31102; NID:g1184272; PIDN:AAB59117.1; PID:g143577
A;Cross-references: EMBL:M31102; NID:g1184272; PIDN:AAB59117.1; PID:g143577
A;Cross-references: EMBL:M31102; NID:g1184272; PIDN:AAB59117.1; PID:g143577
A;Cross-references: EMBL:M31102; NID:g1184272; PIDN:AAB59117.1; PID:g143577
A;Cross-references: EMBL:M31102; NID:g1184272; PIDN:AAB59117.1; PID:g143577
A;Cross-references: EMBL:M31102; NID:g1184272; PIDN:AAB59117.1; PID:g143577
A;Cross-references: EMBL:M31102; NID:g1184272; PIDN:AAB59117.1; PID:g143577
A;Cross-references: EMBL:M31102; NID:g1184272; PIDN:AAB59117.1; PID:g143577
A;Cross-references: EMBL:M31102; NID:g1184272; PIDN:AAB59117.1; PID:g143577
A;Cross-references: EMBL:M31102; NID:g1184272; PIDN:AAB59117.1; PID:g143577
A;Cross-references: EMBL:M31102; NID:g1184272; PIDN:AAB59117.1; PID:g143577
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A;Cros
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A; Title: Sequence of the Bacillus
A; Reference number: S12680; MUID: 9
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A;Experimental source: strain 168
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A; Residues: 1-146 <NAK>
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Superfamily: Escherichia coli ribosomal |
Keywords: protein biosynthesis; ribosome
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98
AEGTEVT
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MUID:90221911
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RESULT 38
C84592
Cypothetical protein At2g20700 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: C84592
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; I
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds; M.; Skelt A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: E87029
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-154 <STO>
A;Cross-references: GB:AL450380; NID:g13093011; PIDN:CAC31344.1; C;Genetics:
G;Genetics: ML0963
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A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-E A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AH1193

A:Crestus resistance
euss, D.; Nierman, W.C.; white, Nature 402, 761-768, 1999
A;Title: Sequence and analysis
A;Reference number: A84420; MUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein [imported] - Mycobacterium leprae C; Species: Mycobacterium leprae C; Species: Mycobacterium leprae C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change C; Accession: E87029 C; Accession: E87029 R; Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, i
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A;Molecule type: DNA
A;Residues: 1-152 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC99030.1;
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: 1mo0952
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C;Date: 27-Nov-2001 #sequence_revision
C;Accession: AH1193
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        MUID: 20083487
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                                                                T.P.; Benito, M.I.; Town, C.D.; Fujii, hen, M.; VanAken, S.E.; Umayam, L.; Tall J.A.; Salzberg, S.L.; Fraser, C.M.; Ven
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J.A.;
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Fsihi, H.
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Holroyd,
                      Eur. J. Biochem. 151, 573-577, 1985
A; Title: Comparison of the nucleotide sequ
A; Reference number: A23117; MUID:85285072
                                                                R; Rhen, M.; van Die, I.; Rhen, V.; Eur. J. Biochem. 151, 573-577, 198
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A; Residues: 1-185 < MA2>
A; Cross-references: EMBL: X61239; |
A; Experimental source: strain J96
C; Genetics:
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A;Map.position: 2
C;Superfamily: Arabidopsis
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N; Alternate names: pap pili
C; Species: Escherichia coli
C; Date: 28-Dec-1987 #sequence_revision 28-De
C; Date: 28-Dec-1987 #sequence_revision 28-De
C; Accession: A23221; $25216; A05229; $16395
R; Baga, M.; Normark, S.; Hardy, J.; O'Hanley
J. Bacteriol. 157, 330-333, 1984
A; Title: Nucleotide sequence of the papa gen
A; Reference number: A91794; MUID:84087728
A; Accession: A23221
A; Molecule type: DNA
A; Residues: 1-185 <BAG>
A; Cross-references: GB:X03391; GB:K01176; GB
R; Marklund, B.I.; Tennent, J.M.; Garcia, E.;
Mol. Microbiol. 6, 2225-2242, 1992
A; Title: Horizontal gene transfer of the Esc
A; Reference number: $25205; MUID:93023852
A; Accession: $25216
                                                                                RESULT 40
YQECKS
YQECKS
KS71A fimbrial protein precursor - Esch
KS71A pilin
C;Species: Escherichia coli
C;Date: 31-Mar-1988 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: papA
C;Superfamily: F7-2 fimbrial protein
C;Keywords: fimbria
F;1-22/Domain: signal sequence #status
F;23-185/Product: fimbrial protein papA
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-181 <STO>
A;Cross-references: GB:AE002093; NID:g445
C;Genetics:
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uences of the genes encoding the KS71A and F
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status predicted <MAT>
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95
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N; Alternate names: F7-2 pilin
C; Species: Escherichia coli
C; Date: 28-Feb-1986 #sequence_revision 28
C; Accession: A03496; B43597
R; Van Die, I.; Bergmans, H.
Gene 32, 83-90, 1984
A; Title: Nucleotide sequence of the gene
A; Reference number: A03496; MUID: 85155489
            C; Genetics:
A; Gene: papA
C; Function:
A; Description:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pilin type F7-1 precursor - Escherichia C; Species: Escherichia coli C; Date: 12-Jan-1993 #sequence_revision C; Accession: C43597 R; Denich, K.; Blyn, L.B.; Craiu, A.; Br Infect. Immun. 59, 3849-3858, 1991
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C43597
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A; Residues: 1-187 <RHE>
A; Cross-references: GB:X02921; NID:g41880; PIDN:CC; Superfamily: F7-2 fimbrial protein
C; Keywords: fimbria
F;1-21/Domain: signal sequence #status predicted
F;22-187/Product: KS71A fimbrial protein #status
                                                                                                              A;Cross-references: GB:M12861; NID:g145963; PR;Denich, K.; Blyn, L.B.; Craiu, A.; Braaten, Infect. Immun. 59, 3849-3858, 1991
A;Title: DNA sequences of three papA genes fra;Reference number: A43597; MUID:92040048
A;Recession: B43597
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YQECF2
                                                                     A; Molecule type: DN:
A; Residues: 1-188 <1
A; Cross-references:
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A; Residues: 1-187 < DEN>
A; Cross-references: GB: M68061; NID: g147072;
C; Superfamily: F7-2 fimbrial protein
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A; Residues: 1-188 < VAN>
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fimbriae,
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fimbrial proteins involved in regulation of phase variation
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MUID:85155489
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86;
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. 86;
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                                                                      PIDN: AAA24278
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RESULT 44
A43597
A43597
pilin type F9 precursor - Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 12-Jan-1993 #sequence_revision 12-Jan-1993 #text_change 26-Aug-1999
C;Accession: A43597
R;Denich, K.; Blyn, L.B.; Craiu, A.; Braaten, B.A.; Hardy, J.; Low, D.A.; O'Hanley, P
Infect. Immun. 59, 3849-3858, 1991
A;Title: DNA sequences of three papA genes from uropathogenic Escherichia coli strain
A;Reference number: A43597
A;Accession: A43597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cysteine synthase (EC 4.2.99.8) cysM [similarity] - Pseudomonas syringae (fragment) N;Alternate names: O-acetylserine (thiol)-lyase B C;Species: Pseudomonas syringae C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 26-May-2000 C;Accession: A41863 R;Hrabak, E.M.; Willis, D.K.
J. Bacteriol. 174, 3011-3020, 1992 A;Title: The lemA gene required for pathogenicity of Pseudomonas syringae pv. syring A;Accession: A41863; MUID:92234961 A;Accession: A41863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-190 <HRA>
A;Residues: 1-190 <HRA>
A;Cross-references: GB:M80477; NID:g151327; PIDN:AAA25875.1; PID:g151328
A;Experimental source: pv. syringae
A;Note: sequence extracted from NCBI backbone (NCBIN:97411, NCBIP:97414)
C;Genetics:
A;Gene: cysM
C;Superfamily: threonine dehydratase
C;Keywords: carbon-oxygen lyase; phosphoprotein; pyridoxal phosphate
F;66/Binding site: pyridoxal phosphate (Lys) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: F7-2 fimbrial protein
C;Keywords: fimbria; mannose-resistant hemagglutination
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-188/Product: F7-2 fimbrial protein #status predicted <MAT>
                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-191 <DEN>
A;Cross-references: GB:M68059;
C;Superfamily: F7-2 fimbrial p
                                                          Query Match
Best Local S
Matches 7
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Best Local S
Matches 7
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VANFNLT
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                                                        Similarity 7; Conserv
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llarity 100.0%;
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protein
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                                                       Score 7; DB 2
Pred. No. 88;
0; Mismatches
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Pred. No. 87;
0; Mismatches
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RESULT 47
$75541
hypothetical protein sll1218 - Synechocys
C; Species: Synechocystis sp.
A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25
C; Accession: $75541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene:
C;Superf
                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-211 <KUR>
A;Cross-references: GB:BA000018; PID:g13702120;
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA2111
                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Kuroda, M.; Ohta, T.; Uchlyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: C90031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein SA2111 [imported] - Staphylococcus aureus (C;Species: Staphylococcus aureus C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change C;Accession: C90031 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Koba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y
DNA Res. 5, 55-76, 1998
A; Title: Complete sequence and gene organization of
A; Reference number: A71000; MUID:98344137
A; Accession: C71022
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C;Species: Pyrococcus horikoshii
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: C71022
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A; Residues: 1-197 <KAW>
A; Cross-references: GB:
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A;Experimental source: strain OT3
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N; Alternate names: collagenase inhibitor; ti. C; Species: Bos primigenius taurus (cattle) C; Date: 16-Nov-1990 #sequence_revision 12-Ap: C; Accession: A35996; A34468; A25322; S28151 R; Boone, T.C.; Johnson, M.J.; De Clerck, Y.A Proc. Natl. Acad. Sci. U.S.A. 87, 2800-2804, A; Title: cDNA cloning and expression of a met A; Reference number: A35996; MUID:90207285 A; Accession: A35996
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A;Gene: ycf39
C;Superfamily:
    possibly controlling their activation; TIC; Superfamily: metalloproteinase inhibitor C; Keywords: erythropoiesis; extracellular F;1-26/Domain: signal sequence #status pre F;27-220/Product: metalloproteinase inhibit;27-98,29-127,39-152,154-201,159-164,172-
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A;Accession: A25322
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A; Residues: 1-219 <KAN>
A; Cross-references: EMBJ
A; Note: the nucleotide:
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A;Title: Sequence analysis of the
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A;Accession: S75541
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K.; Okumura, S.; Shimpo, S.;
lA Res. 3, 109-136, 1996
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tted to the EMBL Data Library, June 1996
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C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
matrix; metalloproteinase inhibitor; mitoge
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itor 2 #status predicted <MAT>
193/Disulfide bonds: #status predicted
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C: Bron, S: Broutllet, S: Bruschi, C:V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choa.

A: Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, Š.; Galizzi, A.; Galler lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A; Cetters, C.; Schikawa, H.; Danchin, A.

A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A; Reference number: A69580; MUID:98044033

A; Accession: C69798
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C; Species: Bacillus subtilis
C; Species: Bacillus subtilis
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C; Accession: C69798
R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedc.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carti
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R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uridylate kinase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
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C69798
                                                                                             A;Experimental source:
C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-231 <ARN>
A;Cross-references: GB:AE001804;
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C;Superfamily: probable membrane protein ycaP
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   A; Gene: TM1604
C; Superfamily:
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A;Title: Evidence
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                                                                                                                                                                                                                                                                                                                                                                                                                          or lateral gene transfer between Archaea and Bacteria from genome see A72200; MUID:99287316
                                                                                                                                              strain
5'-monophosphate kinase
                                                                                                                                       04; GB:AE000512; NID:g4982160; MSB8
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homo sapien	5		ட	950		7	74
haemophilus	P44288	YEBT_HAEIN	Н	881	٠	7	73
human immun	087	ENV_HV1JR	Н	848		7	72
synechocyst	39	PRIA_SYNY3	 -	831	-	7	71
gallus gall	999	CADA_CHICK	μ	789		7	70
apie	9y6n	CADA_HUMAN	ـــر	788		7	69
candida alb	P23316	CHS1_CANAL	ш	776		7	68
rattus norv	P15083	PIGR_RAT	ш	769		7	67
mus musculu	P21180	CO2_MOUSE	Н	760	-	7	66
aquifex aeo	067265	FLHA_AQUAE	щ	678		7	65
arabidopsis	P17597	Г	Н	670		7	64
stylosanthe	P53391	OT1_	Н	667		7	63
_	P47077	YJBO_YEAST	\vdash	666		7	62
homo sapien	Q9by84	DUSX_HUMAN	_	665	•	7	61
stylosanthe	P53392	SUT2_STYHA	Н	662		7	60
5	· P27818	ILV1_BRANA	ب	655	•	7	59
brassica na	P27819	ILV3_BRANA	ш	652	•	7	58
saccharomyc	P53129	YGM4_YEAST	Н	644		7	57
buchnera ap	P57635	PTMA_BUCAI	L	632	٠	7	56
gallus gall	P05153	PPCC_CHICK	ш	622		7	55
schizosacch	Q10190	YAWG_SCHPO	μ	616	•	7	54
saccharomyc	P53306	GPI1_YEAST	<u> </u>	609	•	7	53
Q.	P12374	COPA_PSESM		609		7	52
homo sapien	000178	GTB1_HUMAN	_	584		7	51
-	008582	GTB1_MOUSE	<u> </u>	583		7	50
**	Q14534	ERG1_HUMAN	_	574		7	49
homo sapien	P14778	IL1R_HUMAN	سو	569	•	7	48
achydani	290460	C166_BRARE	\vdash	564	٠	7	47
carassius a	Q90304	16	Н	555	٠	7	46
mus musculu	P16297	IL2B_MOUSE	Н	539	٠	7	45
staphylococ	029	SPA1_STAAU	_	524	•	7	44
aphyl	3850	SPA2_STAAU	بــ	508	•	7	
rattus norv	6272	_		507	•	7	42
O .	9pkk	E H	_	507	•	7	41
mus musculu	073	\mathbf{r}	ب	503		7	
dictyosteli	N	BB_D	_	455	٠	7	9
physarum po	12		۳	454	•	7	
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accharc		¥57_	 .	N	•	7	
ipomoea pur		SB	\vdash	396	0.6	7	35
methanococc		RPA2_METVA	_	œ	•	7	

ALIGNMENTS

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AC P48357;

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-FEB-1996 (Rel. 41, Last annotation update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DT 01-MAR-2002 (Rel. 41, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last sequence update)

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DT 01-MAR-2002 (Rel. 41, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last sequence update)

TEP-ROM OBT.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxiD=9606;

RP SEQUENCE FROM N.A.

PA Mays G.G., Woolf E.A., Morierty A., Moore K.J., Smutko J.S.,

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RA Tartaglia L.A., Dembski M., Weng Y., Deng N., Culpeper J.,

RA Musir C., Sanker S., Morrierty A., Moore K.J., Smutko J.S.,
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"Leptin receptor gene variation and obesity: lack of a white British male population.";
L Hum. Mol. Genet. 6:869-876(1997).
-!- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).
-!- SUBCELLULAR LOCATION: Type I membrano.
-!- SIMILARITY: CONTAINS
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                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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VARIANTS
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MEDLINE-97301763; PubMed-9158141;
Thompson D.B., Ravussin E., Bennett
"Structure and sequence variation at lean and obese Pima Indians.";
Hum. Mol. Genet. 6:675-679(1997).
                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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MEDLINE-97318795; Pubmed-9175732;
Gotoda T., Manning B.S., Goldstone A.I
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MEDLINE-99075638; PubMed-9860295;
Roth H., Korn T., Rosenkranz K., Hinney A., Ziegler A., Kunz J., Siegfried W., Mayer H., Hebebrand J., Grzeschik K.-H.;
"Transmission disequilibrium and sequence variants at the leptin receptor gene in extremely obese German children and adolescents. Hum. Genet. 103:540-546(1998).
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gene (LEPR).";
Diabetes 46:1509-1511(1997).
[6]
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MEDLINE-97431549;
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MEDLINE-96270489;
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Sothern M.,
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Submitted (OCT-1996)
                                                                                                                                                                                                                                                                                te British male population.";
. Mol. Genet. 6:869-876(1997).
FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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7431549; PubMed=9287054;
., Power-Kehoe L., Chua M., Chu F., Udall J.N., Kahle B., Leibel R.
Id intronic sequence variation in
AAA93015.1;
AAB09673.1;
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[3] SEQUENCE FROM N.A. (VARIANTS A TO E). STRAIN-657BL/KS; TISSUE-Hypothalamus; MEDLINE-96231997; PubMed-8628397; Lee G.H., Proenca R., Montez J.M., Carr "Abnormal splicing of the leptin recepto "Abnormal splicing of the leptin recepto "Abnormal splicing of the leptin recepto "Abnormal splicing of the leptin recepto "Abnormal splicing of the leptin recepto "Abnormal splicing of the leptin recepto "Abnormal splicing of the leptin recepto "Abnormal splicing of the leptin recepto "Abnormal splicing of the leptin recepto "Abnormal splicing of the leptin recepto "Abnormal splicing of the leptin recepto "Abnormal splicing of the leptin recepto "Abnormal splicing of the leptin recepto "Abnormal splicing of the leptin recepto "Abnormal splicing of the leptin recepto "Abnormal splicing of the leptin recepto "Abnormal BalbyC: "ISSUE-Hypothalamus; possib hematopolesis and reproduction."; MEDLINE-9620686; PubMed-8616721; Cioffi J.A., Shafer A.W., Zupancic T.J., MEDLINE-9620686; PubMed-89322935; PubMed-8932935; PubMed-8932935; PubMed-8932935; PubMed-8932937; Abnormal splicing by the leptin Percurative STAT signaling by the leptin percurative STAT signaling by the leptin for the pubment of the splicing by the leptin percurative STAT signaling by the leptin percurative STAT signaling by the leptin percurative States and splicing splicing splici
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EMBL; U42467; AAA93014.1; ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).
-!- FUNCTION: THE SHORT FORM (VARIANT A) MAY ACT TO TRANSPORT LEPTIN TO THE CEREBROSPINAL FLUID. THE PUTATIVE SOLUBLE RECEPTOR (VARIA E) COULD FUNCTION AS A TRANSPORT PROTEIN.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXCEPT FOR FORM E WHICH COULD BE SECRETED.
-!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; A, B (SHOWN HERE), C, D AND E; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: (1) VARIANT A: HIGHEST LEVEL OF EXPRESSION I LUNG AND KIDNEY, ALSO PRESENT IN CHOROID PLEXUS AND HYPOTHALAMUS (2) VARIANT B: HIGHEST LEVEL OF EXPRESSION IN HYPOTHALAMUS AND LOWER LEVEL IN BRAIN, TESTES AND ADIPOSE TISSUE. (3) VARIANT E: EXPRESSED IN ADIPOSE TISSUE, HYPOTHALAMUS, HEART, AND TESTES.
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
Reptor; Translive s

1; Alternative s

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187 187
                EXTRACELLULAR (POTENTIAL).

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P97589; O35772;

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SEQUENCE FROM N.A., AND VARIANT FA PRO-2 STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY; MEDLINE-96295531; PubMed-8702432; Iida M., Murakami T., Ishida K., Mizuno "Substitution at codon 269 (glutamine -- receptor (OB-R) cDNA is the only mutatic (fa/fa) rat."; Biochem. Biophys. Res. Commun. 224:597-6
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MEDLINE-96332408; PubMed-8769097;
Takaya K., Ogawa Y., Isse N., Okaz
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TTY; TISSUE+Brain;
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Liabetes 45:1141-1143(1996).

C -!- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).

C -!- FUNCTION: THE SHORT FORM (VARIANT A) MAY ACT TO TRANSPORT LEPT

C -!- FUNCTION: THE SHORT FORM (VARIANT A) MAY ACT TO TRANSPORT LEPT

C -!- SUBCELLULAR LOCATION AS A TRANSPORT PROTEIN.

C -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXCEPT FOR FORM

C -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; A, B (SHOWN HERE), C, D AND

C -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; A, B (SHOWN HERE), C, D AND

C -!- DISEASE: THE FATTY (FA) MUTATION PRODUCES PROFOUND OBESITY OF

C -I- DISEASE: THE FATTY (FA) MUTATION PRODUCES PROFOUND OBESITY OF

C -I- DISEASE: THE FATTY (FA) MUTATION DEFECTIVE NONSHIVERING

THERMOGENESIS, AND PREFERENTIAL DEPOSITION OF ENERGY INTO ADIA

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MEDLINE-96212906;
Iida M., Murakami
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"Analysis
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MEDLINE=96314329; PubMed=8690163;
Chua S.C. Jr., White D.W., Wu-Peng X.S., J. Kershaw E.E., Chung W.K., Power-Kehoe L.,
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STRAIN-SPRAGUE-DAWLEY; TISSUE-Pancrea
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"Molecular cloning of rat DNAs -- identification of
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YTV (IN ISOFORM C).
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C2CA2D2E62AF CRC64;
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STRAIN-ISOLATE ARD 44313;
STRAIN-ISOLATE ARD 44313;
MEDLINE-96332515; Pubmed-8760425;
Marriott A.C., Nuttall P.A.;
"Large RNA segment of Dugbe nairovi polymerase.";
J. Gen. Virol. 77:1775-1780(1996).
                                                                                                                                                                                                                                                                                                                                                                                 RRPL_DUGBV
Q66431;
15-DEC-1998
15-DEC-1998
16-OCT-2001
EMBL; U15018; AAB18834.1; -. InterPro; IPR003323; OTU. InterPro; IPR000822; Znf-C2H2
                                            or send an email to license@isb-sib.ch)
                                                             use by non-profit institutions as modified and this statement is not rementities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-90269039; PubMed-2161319; Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.; "Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Curr. Top. Microbiol. Immunol. 154:125-169(1990).

-!- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER HSV-6
HSV-7 U4, HSV-6 AND HSV-7 U5 AND HCMV UL27.
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[1]
SEQUENCE FROM N.A
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PIR; S09790; S09790.
Hypothetical protein.
SEQUENCE 608 AA; 69220
                                                                                                                                                                                                                                                                                                               NCBI_TaxID=11595;
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Viruses; ss
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Betaherpesvirinae; Cytomegalovirus.
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(Rel. 37, Last sequence update)
(Rel. 40, Last annotation update)
RNA polymerase (EC 2.7.7.48) (L
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                                                                                                                                                                                                                                 of Dugbe nairovirus
                                                                institutions as long as its content tatement is not removed. Usage by an license agreement (See http://www.isb
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P35138;
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                                                                                                                                                                                                                                                                                                                                                                              Ribosomal protein;
NON_TER 1
SEQUENCE 72 AA;
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InterPro; IPR001196; Ribosomal_L15. Pfam; PF00256; L15; 1. PROSITE; PS00475; RIBOSOMAL_L15; 1. Ribosomal protein; rRNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as modified and this statement is not reentities requires a license agreement or send an email to license@isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning and molecular characterization of the secY genes from Bacillus licheniformis and Staphylococcus carnosus: comparative analysis of nine members of the SecY family.";

Mol. Gen. Genet. 235:147-152(1992).

-!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RISOSOMAL RNA.
-!- SIMILARITY: BELONGS TO THE L15P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2685
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PROSITE; PS50802; OTU; 1.

PROSITE; PS00028; ZINC_FINGER_C2H2_1

PROSITE; PS00028; ZINC_FINGER_C2H2_1

Transferase; Nucleotidyltransferase;

DOMAIN 29 158 OTU.

SEQUENCE 4036 AA; 459382 MW; E2E
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Bacteria; Firmicutes; Bacillus/Clost:
Bacillus/Staphylococcus group; Bacil
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RL15_BACSU P19946; 01-FEB-1991

STANDARD;

146 AA.

(Rel.

17, Created)

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Matches 7
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REMBL; X51329; CAA35711.1; -.

REMBL; X51329; CAA35711.1; -.

REMBL; L47971; AAB06818.1; -.

REMBL; M31102; AAB59117.1; -.

REMBL; 299104; CAB11911.1; -.

REMBL; S12682; R5BSL5.

SubtiList; BG10444; rplO.

InterPro; IPR001196; Ribosomal_L15.

Pfam; PF00256; L15; 1.

Refam; PF01305; Ribosomal_L15; 1.

PROSITE; PS00475; RIBOSOMAL_L15; 1.

RIBOSOMAL_L15; 1.

RIBOSOMAL_L15; 1.

SEQUENCE 146 AA; 15383 MW; 5DB07A902B266C11 CRC64;
                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                      "Isolation of a secY homologue from Bacillus subtilis: evidence f common protein export pathway in eubacteria.";

Mol. Microbiol. 4:305-314(1990).

-!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.

-!- SIMILARITY: BELONGS TO THE L15P FAMILY OF RIBOSOMAL PROTEINS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=168 / MARBURG;
MEDLINE=96186897; PubMed=8635744;
Suh J.W., Boylan S.A., Oh S.H., Price C.W.
"Genetic and transcriptional organization
spc-alpha region.";
Gene 169:17-23(1996).
[4]
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Nakamura K., Nakamura A., Takamatsu
"Cloning and characterization of a I
to E. coli secY.";
J. Biochem. 107:603-607(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suh J.-W., Boylan S.A., Thomas Price C.W.;
"Isolation of a secY homologue
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Suh J.-W., Boylan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=90221911; pubMed=2139212;

Yoshikawa H., Doi R.H.;

"Sequence of the Bacillus subtili
region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF
STRAIN-168;
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S.A., Thomas S.M.,
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RESULT 8
CYSM_PSESY
ID CYSM_PSESY
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P48028;
DT 01-FEB-1996 (Rel. 33, Last seque
DT 01-FEB-1997 (Rel. 35, Last annot
DE 01-NOV-1997 (Rel. 35, Last annot
DE (O-accetylserine (Thiol)-lyase B)
CYSM.

OS PSeudomonas syringae (pv. syring
OC Bacteria; Proteobacteria; gamma
OC PSeudomonas.

OX NCBL_TaxID=321;
RN [1]
RP SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
RY MEDLINE-92234961; PubMed-1314807
RA MEDLINE-92234961; PubMed-1314807
RA MEDLINE-92234961; PubMed-1314807
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RA MEDLINE-92234961; PUBMed-1314807
RA MEDLINE-9234961; PALP-
DR HSSP; P12674; 10AS:
DR InterPro; IPR001216; Cys_synthase
DR InterPro; IPR001216; Cys_synthase
DR Lyase; Cysteine biosynthesis; Py
FT BINDING
45 PYF
SEQUENCE 169 AA; 18023 MW; E
RESULT 9
PAPA_ECOLI
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DT 15-DEC
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InterPro; IPR001926; PALP.
Pfam; PF00291; PALP; 1.
PROSITE; PS00901; CYS_SYNTHASE; 1
Lyase; Cysteine biosynthesis; Pyr
BINDING 45 45
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SEQUENCE 169 AA; 18023 MW; E1
  Escherichia.
NCBI_TaxID=562;
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                                                  Escherichia coli.
Bacteria; Proteobacteria;
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MEDLINE-92234961; PubMed-1314807;
Hrabak E.M., Willis D.K.;
"The lemA gene required for patho"
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- CATALYTIC ACTIVITY: O3-acetyl-L's
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COFACTOR: PYRIDOXAL PHOSPHATE.
PATHWAY: CYSTEINE BIOSYNTHESIS.
SIMILARITY: BELONGS TO THE CYSTEIN
SYNTHASE FAMILY.
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EC 4.2.99.8) (O-acetylserine sulfhydrylase B)
1)-lyase B) (CSASE B) (Fragment).
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ily of two-component
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RESULT
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Mol. Microbiol. 6:2225-2242(1992).
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Lindberg F., Gaastra W., Normark S.;
"Horizontal gene transfer of the Escherichia
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Pfam; PF00419; Fimbrial; 1.
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SUBCELLULAR LOCATION: Secreted.

DISEASE: STRAINS OF E.COLI THAT CAUSE INFECTION OF THE HUMAN URINARY TRACT PRODUCE PAP-PILI WHICH ARE HAIR-LIKE APPENDAGES CONSISTING OF ABOUT 1000 HELICALLY ARRANGED SUBUNITS OF THE PROTEIN PAPA. THESE PILI MEDIATE BINDING TO DIGALACTOSIDE-CONTAINING GLYCOLIPIDS PRESENT ON THE EPITHELIAL CELLS WHICH LINE THE URINARY TRACT.

SIMILARITY: BELONGS TO THE FIMA/PAPA FAMILY OF FIMBRIA PROTEINS.
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01-NOV-1995 (Rel. 32, Last annotation
F7-2 fimbrial protein precursor (F7-2,
F7-2 OR PAPA.
"DNA sequences of three papA genes f. coli strains: evidence of structural Infect. Immun. 59:3849-3858(1991).
-!- FUNCTION: FIMBRIAE (ALSO CALLED | FROM THE SURFACE OF THE BACTERIUM MICROMETERS AND NUMBERING 100-30)
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SEQUENCE FROM N.A.
MEDLINE-85285072; PubMed-2992970;
Rhen M., van Die I., Rhen V., Bergmans H.;
"Comparison of the nucleotide sequences of the genes encoding the KS71A and F7(1) fimbrial antigens of uropathogenic Escherichia
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FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5
MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.
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P16368
DT 01-AUG
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DE Metall
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RN [1]
RP SEQUEN
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Matches 7
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Mammalia; Eutheria
Bovidae; Bovinae; I
NCBI_TaxID~9913;
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EMBL; M68060;
PIR; A03496; Y
PIR; B43597; B
                                                                                                                                                                                                                                                      Submitted [3] SEQUENCE O
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SEQUENCE
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Fimbria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90207285; PubMed=2157214;
Boone T.C., Johnson M.J., de Clerck Y.A., Langley K.
"cDNA cloning and expression of a metalloproteinase
to tissue inhibitor of metalloproteinases.";
Proc. Natl. Acad. Sci. U.S.A. 87:2800-2804(1990).
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p16368; 09TVB1;
01-AUG-1990 (Rel. 15, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Metalloproteinase inhibitor 2 precursor (TIMP-2)
metalloproteinases-2) (Collagenase inhibitor).
                                                                SEQUENCE OF 27-71.

TISSUE-Cartilage;

MEDLINE-86140235; PubMed-3005321;

Murray J.B., Allison K., Sudhalter J.

"Purification and partial amino acid derived collagenase inhibitor.";
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                                                                                                                                                                                                                                                                                                                         Balcerzak D., Querengesser L., Dixon W.T., Baracos V.E.; "Involvement of fibroblasts and muscle cells in the expression extracellular proteolytic cascade in bovine skeletal muscle."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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MEDLINE-90207285; Pu
Boone T.C., Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
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                                          Biol.
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- DISEASE: THIS IS ONE
MANNOSE-RESISTANT HEM
- SIMILARITY: BELONGS T
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Pro; IPR000259; Fimbrial.
PF00419; Fimbrial; 1.
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Similarity 100.0%;
7; Conservative
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                                          Chem.
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43
188 /
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; AAA24278.1;
YQECF2.
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THIS IS ONE OF THE FIMBRIAL PROTEINS INVOLVED IN
RESISTANT HEMAGGLUTINATION OF HUMAN ERYTHROCYTES.
FY: BELONGS TO THE FIMA/PAPA FAMILY OF FIMBRIA PRO
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                                          261:4154-4159(1986)
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188
82
19184
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Pred. No. 36;
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OEEF750CFD843157
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RESULT 13
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Matches 7
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Pfam; PF00965; TIMP; 1.
SMART; SM00206; TIMP; 1.
PROSITE; PS00288; TIMP; 1.
Metalloprotease inhibitor; S
SIGNAL 1 27 220
DISULFID 27 98
DISULFID 29 127
DISULFID 39 152
DISULFID 39 152
DISULFID 154 201
DISULFID 154 201
DISULFID 159 164
DISULFID 172 193
CONFLICT 42 42
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CONFLICT 66 66
CONFLICT 66 68
SEQUENCE 220 AA; 24355 MW
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EMBL; AF144764; AAD30304.1; -
PIR; A25322; A25322.
PIR; A35996; A35996.
PIR; A34468; A34468.
HSSP; P16035; 1BR9.
                                                                                                                                                                                                             PYRH_THEMA STANDARD;
Q9X1U0;
16-OCT-2001 (Rel. 40, Cr
16-OCT-2001 (Rel. 40, La
16-OCT-2001 (Rel. 40, La
Uridylate kinase (EC 2.7
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MEDLINE-90008914; P
de Clerck Y.A., Yea
"Purification and c
Bacteria; Thermotoc
NCBI_TaxID=2336;
[1]
SEQUENCE FROM N.A.
STRAIN=MSB8 / DSM:
MEDLINE=99287316; I
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                                                                                                                       Thermotoga Bacteria; '
                                                                                                                                                                (UMP kinase).
PYRH OR TM1604.
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FUNCTION: COMPLEXES WITH METALLOPS
AND IRREVERSIBLY INACTIVATES THEM
SUBCELLULAR LOCATION: Secreted.
PTM: THE ACTIVITY OF TIMP-2 IS DES
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SIMILARITY: BELONGS
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Thermotogales;
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ean T.D., Ratzkin
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8737110E7B7 CRC64;
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No. 41;
atches
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Best Local S
Matches 7
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P38727;
01-FEB-1995 (Rel. :
01-FEB-1995 (Rel. :
16-OCT-2001 (Rel. :
Hypothetical 27.0)
YHL044W.
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                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
MEDLINE-94378003; PubMed-8091229;
Johnston M., Andrews S., Brinkman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A., McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.; "Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima."; Nature 399:323-329(1999).

-I- FUNCTION: URIDINE MONOPHOSPHATE KINASE (BY SIMILARITY).
-I- CATALYTIC ACTIVITY: ATP + UMP = ADP + UDP.
-I- SIMILARITY: TO OTHER UMP KINASE; SOME, TO ASPARTOKINASES AND TO GLUTAMATE KINASES.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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TIGR;
                                                                                                                                                                                                Science
                                                                                                                                                                                                                        VIII."
                                                                                                                                                                                                                                                                           Vaudin M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Saccharomyc. Saccharomycetales; Saccharomycetaceae; Sancharomycetaceae; Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1049
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Pfam; PF00696; aakinase; 1.
Transferase; Kinase; Pyrimidir
SEQUENCE 231 AA; 25235 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ELLULAR LOCATION: Integral
LARITY: BELONGS TO THE DUP
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Similarity 100.0%;
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31,
40,
kDa
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25235 MW; 4
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protein in CBP2 5'region.
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Pred. No. 43;
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4563E9E15FA0C5ED
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Geisel C., Kirsten
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Matches
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Duesterhoeft A., Floeth M., Fri
Moestl D.;

Submitted (MAY-1996) to the EME
-!- CATALYTIC ACTIVITY: ATP + 7

Phosphate + dethiobiotin.
-!- COFACTOR: MAGNESIUM.
-!- PATHWAY: BIOCONVERSION OF F
-!- SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical |
TRANSMEM
TRANSMEM
SEQUENCE 23
NP_BIND
SEQUENCE
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PIR; ;
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                                                                                                                                                                                                                                                                                                                                                                                                                               BIOD_YEAST STANDARD; PRT; 2
P53630;
P53630;
O1-OCT-1996 (Rel. 34, Created)
O1-OCT-1996 (Rel. 34, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Dethiobiotin synthetase (EC 6.3.3.3.3)
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                       SGD; S0005340; BIO4.
Biotin biosynthesis; Ligase;
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STRAIN-FL100;
Phalip V., Jeltsch J.M.,
Submitted (MAY-1996) to
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                           synthetase) (DTBS).
BIO4 OR YNR057C OR N3506.
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Pfam; PF00674; DUP;
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271672; CAA96339.1;
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THE DETHIOBIOTIN SYNTHETASE FAMILY.
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+ 7,8-diaminononanoate + CO(2) =
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Magnesiu
ATP (BY
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um; ATP-binding.
SIMILARITY).
BF18DA40735 CRC64;
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(See http://www.isb-sib.ch/announce/
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Length 237;

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P71772;
O1-NOV-1997 (Rel. 35, Created)
O1-NOV-1997 (Rel. 35, Last sequence upda
16-OCT-2001 (Rel. 40, Last annotation up
Hypothetical 26.6 kDa protein Rv1491c.
RV1491C OR MT1538 OR MTCY277.13C.
Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Ac
Actinomycetales; Corynebacterineae; Myco
                                                                                                                                             Hypothetical TRANSMEM TRANSMEM
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                                                                        TRANSMEM TRANSMEM SEQUENCE
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                  TRANSMEM TRANSMEM
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EMBL;
TIGR;
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                                                                                                                                                                                                                                                                                                                                                                       "Whole genome comparison of Mycobacterium tuberculosis claboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Pot-
-!- SIMILARITY: BELONGS TO THE UPF0043 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E. Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
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Similarity 100.0%;
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MEDLINE=95324575; PubMed=7601147;

van der Palen C.J., Slotboom D.J., Jongejan L., Reijnders W Harms N., Duine J.A., van Spanning R.J.;

"Mutational analysis of mau genes involved in methylamine m in Paracoccus denitrificans.";

Eur. J. Biochem. 230:860-871(195).

-!- FUNCTION: INVOLVED IN ELECTRON TRANSFER (POTENTIAL).

-!- PATHWAY: METHYLAMINE UTILIZATION.

-!- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOS:

'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.
                                                                                                                                                                                                                      Matches
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HSSP; P00195; 1CLF.
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PDB; 1EXN; 07-JUL-97.

PDB; 1XO1; 12-APR-99.

InterPro; IPR002421; 5_3_exonuclease.

InterPro; IPR000513; Exo_N_I.

InterPro; IPR000513; Exo_N_I.

InterPro; IPR003584; HHH_2.

Pfam; PF01367; 5_3_exonuclease; 1.

SMART; SM00475; 53EXOC; 1.

SMART; SM00279; HhH2; 1.
 NPL_HAEIN
P44539;
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SEQUENCE
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MEDLINE-86108899; PubMed-3002857;

Kaliman A.V., Krutilina A.I., Kryukov V.M., Baye "Cloning and DNA sequence of the 5'-exonuclease T5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cleavage.";
Proc. Natl. Acad. Sci. U.S.A. 96:38-43(1999).
-I- CATALYTIC ACTIVITY: DEGRADATION OF DOUBLE-STRANDED STRANDED DNA. IT ACTS PROGRESSIVELY IN A 5' TO 3' E RELEASING 5'-PHOSPHOMONONUCLEOTIDES.
-I- COFACTOR: REQUIRES DIVALENT CATIONS FOR ACTIVITY.
-I- SIMILARITY: CONTAINS 1 5'-3' EXONUCLEASE DOMAIN.
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PIR; /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriophage T5.
Viruses; dsDNA viruses,
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Nature 382:90-93(1996).
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MEDLINE-96273035; PubMed-8657312;
Ceska T.A., Sayers J.R., Stier G., Suck D.;
"A helical arch allowing single-stranded DNA to exonuclease.";
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Exodeoxyribonuclease (EC 3.1.11.3) (5' exonuc
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YCJY_ECOLI
Y76049; P77483; P76844;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last seque
16-OCT-2001 (Rel. 40, Last annot
Hypothetical protein ycjY.
YCJY OR B1327.
                                                                                                                                                                                                                                                                                                                             EMBL; U32700; AAC21814.1; -.
HSSP; P06995; 1NAL.
TIGR; HI0142; -.
InterPro; IPR002220; DHDPS.
Pfam; PF00701; DHDPS; 1.
PRINTS; PR00146; DHPICSNTHASE.
PRODOm; PD001859; DHDPS; 1.
PROSITE; PS00665; DHDPS_1; 1.
PROSITE; PS00666; DHDPS_2; 1.
LYase; Complete proteome.
ACT_SITE 164 164 BY
SEQUENCE 293 AA; 32564 MW;
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STRAIN=RD / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F.; Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Scott J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

"Whole-company"
                                                                                                                                                                                                                                1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Whole-genome random sequencing and influenzae Rd.";
Science 269:496-512(1995). |
-!- CATALYTIC ACTIVITY: N-acetylneur.
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NANA OR H
  Bacteria; P
Escherichia
                            Escherichia coli.
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Bactería; Proteobactería;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pyruvate.
SUBUNIT: HOMOTRIMER (BY SIMILARI
SIMILARITY: BELONGS TO THE DHDPS
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               Proteobacteria;
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cetylneuraminate pyruvate lyase)
            ivision;
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5D0A5D93D33 CRC64;
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               Enterobacteriaceae;
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A Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,

A Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,

A Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori J.

A Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,

A Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S.,

Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,

A Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,

A Yamamoto Y., Horiuchi T.;

T "A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map."

L DNA Res. 3:363-377(1996).

C -1- SIMILARITY: TO P.AERUGINOSA HYPOTHETICAL 40.7 kDa PROTEIN 3'REGION (AC Q01609).
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 7
                                                                                                                           SULT 21
11_YEAST
PP11_YEAST STANDARD; PRT; 311 AA.
P20604;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Serine/threonine protein phosphatase PP1-1 (EC)
PPH1 OR SIT4 OR VDL047W OR D2693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000230; AAC74409.1; -.
EMBL; D90770; BAA14909.1; -.
EMBL; D90771; BAA14920.1; -.
EMBL; D90772; BAA14930.1; -.
EcoGene; EG13922; ycjr.
InterPro; IPR000379; Est_lip_thioest_actsite.
Hypothetical protein; Complete proteome.
CONFLICT 259 259 S-> R (IN REF. 2)
SEQUENCE 310 AA; 34117 MW; 20291A71BD367B70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-K12;
MEDLINE-97251357; PAiba H., Baba T., Fitoh T., Kasai H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-K12 / MG1655;

MEDLINE-97426617; PubMed-9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;

"The complete genome sequence of Escherichia coli K-12.";
SEQUENCE FROM N.A. MEDLINE-89136000; I
                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Saccharor
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science
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Similarity 100.0%;
7; Conservative
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 PubMed-2537149;
s C.A., Fink G.R.
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Pred. No. 55;
0; Mismatches
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-> R (IN REF. 2)
20291A71BD367B70
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PP1-1 (EC
                                                                                   sycotina; Saccharomycetes;
Saccharomyces.
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io Y.,
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EMBL; Z71781; CAA96442.1; -.
EMBL; Z74095; CAA98609.1; -.
PIR; A31874; PABY1.
HSSP; P08129; 1FJM.
SGD; S0002205; SIT4.
InterPro; IPR000934; Ser_thr_phosphtse.
Pfam; PF00149; STphosphatase; 1.
PRINTS; PR00114; STPHPHTASE.
SMART; SM00156; PP2Ac; 1.
PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detween the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE
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METAL
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Sutton A., Immanuel D., Arndt K.T.;
"The SIT4 protein phosphatase functions in late G1 for progression into S phase.";
Mol. Cell. Biol. 11:2133-2148(1991).
-i- FUNCTION: INVOLVED IN THE DEPHOSPHORYLATION OF THE LARGE SUBUNIT OF RNA POLYMERASE II. IS REQUIRED IN LATE G1 FOR NORMAL G1 CYCLIN EXPRESSION, BUD INITIATION AND EXPRESSION OF CERTAIN GENES THAT ARE PERIODICALLY EXPRESSED DURING LATE G1. ASSOCIATES WITH THE SAP PROTEINS IN A CELL CYCLE-DEPENDENT MANNER.
-i- CATALYTIC ACTIVITY: A phosphoprotein + H(2)0 = a protein +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A suppressor of a HIS4 transcrine homology to the catalytic subunicell 56:527-537(1989).
[2] SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION. MEDLINE-91172202;
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SIMILARITY:
SUBFAMILY.
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SUBCELLULAR LOCATION: Cytoplasmic.
SUBCELLULAR LOCATION: Cytoplasmic.
DEVELOPMENTAL STAGE: FUNCTIONS IN
PROGRESSION INTO THE S PHASE, POSS
COMPLEXES WITH THE PHOSPHORYLATED
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                                                                                                                                                                                                                                       Similarity 100.0%; 7; Conservative
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82
114
115
164
238
311 AV
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                                                                                                                                                                                                                                                                                                                                                               AA;
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AA; 35537 MW
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) the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                     . 68
                                                                                                                                                                                                                                                                                                                                                        e; Cell cycle; Mitosis; Multigene family.
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON AND MANGANESE (BY SIMILARITY).
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subunit of p
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A Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
A Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
A Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
A Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
A Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.
A Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
A Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
A Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
A Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
A Venter J.C.;
T "The complete genome sequence of the hyperthermophilic, sulphate-
T reducing archaeon Archaeoglobus fulgidus.";
L Nature 390:364-370(1997).
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RCC1_SCHPO STANDARD; PRT; 335 AA.

Q9P7I2; 074235;

P 16-OCT-2001 (Rel. 40, Created)

P 16-OCT-2001 (Rel. 40, Last sequence update)

P 16-OCT-2001 (Rel. 40, Last annotation update)

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Hypothetical protein; Transme TRANSMEM 13 35
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SEQUENCE 329 AA; 37776 MW;
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                             SEQUENCE FROM N.A., SUBCELLULAR LOCATION, MEDLINE-20085094; PubMed-10617667; Rasmussen C.D.;
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STRAIN-VC-16 / DSM 4304 / ATCC 49558;

MEDLINE-98049343; PubMed-9389475;
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STRAIN-972;

Wood V., Rajandream M.A., Barrell B.G.

Submitted (FEB-2000) to the EMBL/GenBa-
-!- FUNCTION: IMPORTANT IN CELL CYCLE
-!- CATALYTIC ACTIVITY: ATP + protein
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE SER/THR
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EMBL; AL157993; CAB76233.1; -.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR0002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS00111; PROTEIN_KINASE_DOM; PROTEIP; PS00111; PROTEIN_KINASE_ST; 1
ATP-binding; Serine/threonine-protein }
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P94929;

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Han M.Y., Son M.Y., I
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                                                                                                                                                                                               Bacteria; Firmicutes; Actinomycetales; Cory, NCBI_TaxID=1765;
                                                                                                                                               SEQUENCE
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. 37, Last sequence up
. 37, Last annotation
e dehydrogenase (EC 1
                                                                                                                                                                                                                                   Corynebacterineae;
                                                      PubMed=9111927;
Lee S.H., Kim
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IN CELL CYCLE REGULATION.
ATP + protein = ADP + 0-ph/
N: Cytoplasmic.
TO THE SER/THR
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xn update)
1.1.1.85) (Beta-IPM dehydrogenase)
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                                                                                                                                                                                                                                 , Actinobacteridae;
Mycobacteriaceae; Mycobacterium.
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SIMILARITY)
LIN-BINDING (POTENTIAL).
                                                      K., Huh J.S., Kim J.H., Choe I.S.,
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BCFF6882B02 CRC54;
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5-FOLD INCREASE IN ACTIVITY.
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    from Mycobacterium bovis BCG and
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. 59;
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RESULT
SEQUENCE FROM N.A.

C STRAIN-H37RV;

C MEDLINE-98295987; PubMed-9634230;

X MEDLINE-98295987; PubMed-9634230;

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X MEDLINE-98295987; PubMed-9634230;

X MEDLINE-98295987; PubMed-9634230;

X MEDLINE-98295987; PubMed-9634230;

X MEDLINE-98299987; PubMed-9634230;

X Medline-T., Churcher C., Harris D.,

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X Medline-T., Chillingworth T., Churcher C., Harris D.,

X Medline-T., Churcher C., Harris D.,

X Medline-T., Chillingworth T., Chillingworth T., Connor R.,

X Medline-T., Connor R., Holroyd S.,

X Medline-T., Chillingworth T., Chillingworth T., Connor R.,

X Medline-T., Connor R., Holroyd S.,

X Medline-T., Chillingworth T., Chillingworth T., Connor R.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEU3_MYCTU STANDARD; PRT; 336 AA. P95313; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 3-isopropylmalate dehydrogenase (EC 1.1.1.85) (IMDH) (3-IPM-DH). LEUB OR RV2995C OR MT3073 OR MTV012.09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U78886; AAC45173.1; -.
HSSP; P00351; 1XAA.
InterPro; IPR001804; Isodh.
Pfam; PF00180; isodh; 1.
PROSITE; PS00470; IDH_IMDH; 1.
Oxidoreductase; Leucine biosynthesis; NAD.
SEQUENCE 336 AA; 35272 MW; 03C95850A6CA51E2
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97266124; PubMed-9111927;
Han M.Y., Son M.Y., Lee S.H., Kim J.K., Hu. Chung T.W., Choe Y.K.;
"Molecular cloning of the leuB genes from I Mycobacterium tuberculosis.";
Biochem. Mol. Biol. Int. 41:657-663(1997).
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Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Corynebacterineae; M
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NCBI_TaxID=1773;
[1]
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chem. Mol. Biol. Int. 41:657-663(1997).
CATALYTIC ACTIVITY: 3-CARBOXY-2-HYDROXY-4-METHYLPENTANCATE
NAD(+) = 3-CARBOXY-4-METHYL-2-OXOPENTANOATE + NADH (THE PRO
DECARBOXYLATES TO 4-METHYL-2-OXOPENTANOATE).
PATHWAY: THIRD STEP IN LEUCINE BIOSYNTHESIS.
SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE
DEHYDROGENASES FAMILY.
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larity 100.0%;
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Pred. No. 59;
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RESULT 26
GGH_SOYBN
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EMBL; AL021287; CAA16080.1; -.
EMBL; AE007127; AAK47402.1; -.
HSSP; P00351; 1XAA.
TIGR; MT3073; -.
TubercuList; Rv2995c; -.
InterPro; IPR001804; Isodh.
Pfam; PF00180; Isodh; 1.
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[3]
SEQUENCE FROM N.A.
STORATN-CDC 1551 / C
                                                                                                              GGH_SOYBN STANDARD; PRT; .342 AA.

P93164;

15-JUL-1999 (Rel. 38, Created)

15-JUL-1999 (Rel. 38, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)

15-JUL-1999 (Rel. 38, Last annotation update)

Gamma-glutamyl hydrolase precursor (EC 3.4.19.9) (Gamma-GLU-X carboxypeptidase) (Conjugase) (GH).

Glycine max (Soybean).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

NCBI_TaxID-3847;
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between
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: 3-CARBOXY-2-HYDROXY-4-METHYLPENTANOATE NAD(+) = 3-CARBOXY-4-METHYL-2-OXOPENTANOATE + NADH (THE PROCARBOXYLATES TO 4-METHYL-2-OXOPENTANOATE).
-!- PATHWAY: THIRD STEP IN LEUCINE BIOSYNTHESIS.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fleischmann R.D., Alland D., Eisen Peterson J., DeBoy R., Dodson R., (Kolonay J.F., Nelson W.C., Umayam I Delcher A., Utterback T., Weidman
                                           SEQUENCE FROM N.A.
STRAIN=CV. WILLIAMS 82;
MEDLINE=97069645; PubMed=8912628;
Huangpu J., Pak J.H., Burkhart W.,
                                Huangpu J., Graham J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00180; isodh; 1.
PROSITE; PS00470; IDH_IMDH; 1.
Oxidoreductase; Leucine biosynthesis;
SEQUENCE 336 AA; 35306 MW; E787181
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                  "Purification
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Swinn M.L., Haft D., Hickey E.,
L.A., Ermolaeva M.D., Salzberg S.L.,
J., Khouri H., Gill J., Mikula A.,
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STRAIN=K12;

MEDLINE=97251357; PubMed=9097039;

Miba H., Baba T., Fujita K., Hayashi K., Inada Aiba H., Baba T., Fujita K., Kimura S., Kitakawa M. Kasai H., Kashimoto K., Kimura S., Kitakawa M. Makino K., Miki T., Mizobuchi K., Mori H., Mor Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Nashimoto G., Seki Y., Sivasundaram S., Tagami H.
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P24213; P77676;
01-MAR-1992 (Rel. 2
01-NOV-1997 (Rel. 3
16-OCT-2001 (Rel. 4
Possible protease s
SOHB OR B1272.
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SIGNAL 1
CHAIN 22
CARBOHYD 72
SEQUENCE 342 AA;
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STRAIN-K12 / MG1655;
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
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-!- CATALYTIC ACTIVITY: Cleavage of a gamma-glutamyl an unsubstituted C-terminal amino acid.

-!- SUBCELLULAR LOCATION: EXTRACELLULAR OR CELL-WALL-
-!- TISSUE SPECIFICITY: EXPRESSED ONLY IN YOUNG (1-15 STEM AND ROOT TISSUE.

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C26.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=91358368; PubMed=1885549;

Baird L., Lipinska B., Raina S., Georgopoulos C.;

"Identification of the Escherichia coli sohB gene, suppressor of the HtrA (DegP) null phenotype.";

J. Bacteriol. 173:5763-5770(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli.
Bacteria; Proteobacteria;
Escherichia.
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, Goeden M.A., Rose D.J.
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Fleischmann R.D., Adams M.D., White O., Kerlavage A.R., Bult C.J., Tomb J.-F., McKenney K., Sutton G., Fitzhugh W., Fi Scott J.D., Shirley R., Liu L.-I., Gloc Weidman J.F., Phillips C.A., Spriggs T. Utterback T.R., Hanna M.C., Nguyen D.T. Fine L.D., Fritchman J.L., Fuhrmann J.I. Gnehm C.L., McDonald L.A., Small K.V., Venter J.C.;
"Whole-genome random sequencing and assinfluenzae Rd.";
Science 269:496-512(1995).
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-!- FUNCTION: MULTICOPY SUPPRESSOR OF 'IT IS POSSIBLY A PROTEASE, NOT ESSI IT IS POSSIBLY A PROTEASE, NOT ESSI SIMILARITY: BELONGS TO PEPTIDASE FACE
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-F., Dougherty B.A., Merrick J.M.,
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19s T., Hedblom E., Cotton M.D.,
1 D.T., Saudek D.M., Brandon R.C.,
1 D.T., Geoghagen N.S.M.,
(.V., Fraser C.M., Smith H.O.,
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Pfam; PF01343; Peptidase_U7; 1.

ProDom; PD002897; Peptidase_U7; 1.

Protease; Hydrolase; Transmembrane; Complete pr
TRANSMEM 11 31 POTENTIAL.

SEQUENCE 353 AA; 39872 ***
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-95241498; PubMed-7724563;
Durbin M.L., Learn G.H., Huttley G.P.
Perolution of the chalcone synthase
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p48396;

01-FEB-1996 (Rel. 33, Created)

01-FEB-1996 (Rel. 33, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)

Chalcone synthase B (EC 2.3.1.74) (Naringenin-chalcone (CHS-B) (Fragment).
    EMBL; (
InterPi
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Eukaryota; V1ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.
NCBI_TaxID=35883;
                                                                                       use by non-profit institutions as modified and this statement is not rementities requires a license agreement or send an email to license@isb-sib.cl
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NARINGENIN.

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CATALYTIC ACTIVITY: 3 malonyl-CoA + 4-coumarcy carringenin-chalcone + 3 CO(2).

PATHWAY: PART OF THE BIOSYNTHETIC PATHWAY FOR FLAVONOIDS, A LARGE CLASS OF SECONDARY PLANT MOF WHICH ARE BRIGHTLY COLORED.

SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE/STILBENE SECONDARY PLANT MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHALCONE MORE CHAL
                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collabween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for contities requires a license agreement (See http://www.isb-sib.ch/ar
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WHICH CAN UNDER SPECIFIC CONDITIONS SPONTANEOUSLY ISOMERIZE
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Best Loc
Matches
Fan H.Y., Mao Y.F., Dai M., Huang Q.H., "Human partial CDS from cd34+ stem cells Submitted (MAY-1999) to the EMBL/GenBank, i- FUNCTION: DOES NOT HAVE CYCLASE ACTIVE RIBOSOMAL-SUBUNIT BIOGENESIS IN THE I STEPS AT SITES A0, A1 AND A2 THAT ARE MATURATION OF THE 185 RNA (BY SIMILAR I-- SIMILAR LOCATION: NUCLEAR; NUCLEO- I- SIMILARITY: BELONGS TO THE RNA 3'-TER SUBFAMILY 2.
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Q9Y2P8; Q9NY00; Q9P044; Q9H9D0;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence updat
16-OCT-2001 (Rel. 40, Last annotation upd
RNA 3'-terminal phosphate cyclase-like pr
RNAC OR RPC2 OR RTC2 OR RCL1.
Homo sapiens (Human).
                                                                                                                                                                                                                                      SEQUENCE OF 46 TISSUE-Blood; Ye M., Zhang C
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ACT_SITE
NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 8-373 FROM N.A.
Kan L., Zhang Q.H., Fu G., Zhou J
Chen S.J., Mao M., Chen Z.;
"Human hematopoietic cell derived
submitted (MAY-1998) to the EMBL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Billy E., Wegierski T., Nasr F., F. Rcllp, the yeast protein similar associates with U3 snoRNP and is rembo J. 19:2115-2126(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (NOV-2000)
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MEDLINE-20253086; PubMed-10790377;

MEDLINE-20253086; PubMed-10790377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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                                                                                                         Wu X.Y., Guen Z.Q., Wang L., H., Chen S.J., Chen Z.;

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THE EARLY PRE-RRNA PROCESSING
ARE REQUIRED FOR PROPER
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the RNA 3'-phosphate cyclase,
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kahashi-Fujii A., Hara H.,
i F., Hara R., Takeuchi K.,
i Y., Saito K., Yamamoto J.,
., Masuho Y., Oshima A.;
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63;
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.; Hominidae; Homo.
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SEQUENCE FROM N.A.

P SEQUENCE FROM N.A.

C STRAIN-C57BL/6J; TISSUE-Tongue;

C MEDLINE-21085660; PubMed-11217851;

X MEDLINE-21085660; PubMed-11217851;

X MEDLINE-21085660; PubMed-11217851;

X MEDLINE-21085660; PubMed-11217851;

X MEDLINE-21085660; PubMed-11217851;

X MEDLINE-21085660; PubMed-11217851;

X MARAWA T., Shinagawa A., Stohia Y., Konno H., Adachi J., Fukuda S.,

X A Arakawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Saito R.,

X A Arakawa T., Saito R.,

X A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

X A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

X A Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

X A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

X A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

X A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

X A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

X Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

B Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
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Best Local S
Matches 7
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Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Rodentia; S

NCBI_TaxID=10090;

[1]
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EMBL; BC001025; AAH01025.1; --
EMBL; AK022904; BAB14300.1; --
EMBL; AF067172; AAD32456.1; A
EMBL; AF161456; AAF29016.1; --
InterPro; IPR000228; RTC.
Pfam; PF01137; RTC; 1.
PROSITE; PS01287; RTC; 1.
Nuclear protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9JJTO;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
RNA 3'-terminal phosphate cyclase-like protein.
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE-20253086; PubMed-10790377;

Billy E., Wegierski T., Nasr F., Filipowicz W.;

"Rcllp, the yeast protein similar to the RNA 3'-phosphate cyclase,

associates with U3 snoRNP and is required for 18S rRNA biogenesis.";

EMBO J. 19:2115-2126(2000).
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between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
use by non-profit institutions as long as its content is
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D -> S (IN REF. 5).
A -> S (IN REF. 5).
K -> N (IN REF. 3).
R -> Q (IN REF. 2 AND 3).
51EFAC56F0AF93CB CRC64;
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16-OCT-2001
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EMBL; AK009709; BAB26454.1; -.
MGD; MGI:1913275; Rnac.
InterPro; IPR000228; RTC.
Pfam; PF01137; RTC; 1.
PROSITE; PS01287; RTC; 1.
Nuclear protein.
SEQUENCE 373 AA; 40840 MW; 3
Cotton M.D., Roberts K.M., Klenk H.-P., Fraser C.M., Somplete genome sequence of jannaschii.";
Science 273:1058-1073(1996)
[2]
SIMILARITY.
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou Sutton G.G., Blake J.A., FitzGerald I Sutton G.G., Blake J.A., Tomb
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                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea; Euryarchaeota; Methanococcus. NCBI_TaxID=2190;
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Nature 409:685-690(2001).
-!- FUNCTION: DOES NOT HAVE CYCLASE ACTIVITY. PLAYS A ROLE IN A
RIBOSOMAL-SUBUNIT BIOGENESIS IN THE EARLY PRE-RNA PROCESS!
STEPS AT SITES AO, AI AND A2 THAT ARE REQUIRED FOR PROPER
MATURATION OF THE 18S RNA (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE RNA 3'-TERMINAL CYCLASE FAMILY.
SUBFAMILY 2.
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Suzuki H., Toyo-oka K., Wang K.H., W
Wynshaw-Boris A., Yoshida K., Hasega
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1 (Rel. 40, Last annotate)
2al ATP-binding protein N
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L.M., Clayton R.A., Gocayne J.D.,
J.-F., Adams M.D., Reich C.I.,
k K.G., Merrick J.M., Glodek A.,
n J.F., Fuhrmann J.L., Nguyen D.,
n J.D., Sadow P.W., Hanna M.C.,
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                                                                                                ., Kaine B.P., Borodovsky M.,
, Woese C.R., Venter J.C.;
nanogenic archaeon, Methanococcus
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Best Local S
Matches
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PURT_BACSU STANDARD,

P39771; O31450;

01-FEB-1995 (Rel. 31, Created)

15-DEC-1998 (Rel. 37, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Phosphoribosylglycinamide formyltransferase 2 (EC 2.1)

(GAR transformylase 2) (5'-phosphoribosylglycinamide)

(GAR transformylase).
        Haga K., Liu H., Yasumoto K., Takahashi H., Yoshikawa H.;

"Sequence analysis of the 70kb region between 17 and 23 degree of the Bacillus subtilis chromosome.";

Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: CATALYZES TWO REACTIONS:THE FIRST ONE IS THE PRODUCTION OF BETA-FORMYL GLYCINAMIDE RIBONUCLEOTIDE (GAR) FROM FORMATE, ATP AND BETA GAR; THE SECOND, A SIDE REACTION, IS THE PRODUCTION OF ACETYL PHOSPHATE AND ADP FROM ACETATE AND ATP.

-!- CATALYTIC ACTIVITY: FORMATE + ATP + 5'-PHOSPHO-RIBOSYLGLYCINAMIDE - 5'-PHOSPHORIBOSYL-N-FORMYLGLYCINAMIDE + ADP + PYROPHOSPHATE.

-!- COFACTOR: MAGNESIUM (BY SIMILARITY).

-!- PATHWAY: THIRD STEP (FIRST OF TWO TRANSFORMYLATION REACTIONS)

IN DE NOVO PURINE BIOSYNTHESIS. THIS IS AN ALTERNATIVE ENZYME TO
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Pfam; PF01637; Archaeal_ATPase; 1.
ProDom; PD003808; Archaeal_ATPase; 1.
ProDom; PD003808; Archaeal_ATPase; 1.
ProDom; PD003808; Archaeal_ATPase; 1.
Pypothetical protein; ATP-binding; Cc.
NP_BIND 29 36 ATP (POTE NP_BIND 29 36 ATP (POTE NP_BIND 29 36 ATP (POTE NP_BIND 29 36 ATP (POTE NP_BIND 29 36 ATP (POTE NP_BIND 29 36 ATP (POTE NP_BIND 29 379 AA; 44716 MW; 1BAF25
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Saxild H.H., Jacobsen J.H., Nygaard P.;
"Functional analysis of the Bacillus subtilis
formate-dependent glycinamide ribonucleotide of
Microbiology 141:2211-2218(1995).
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Bacteria; Firmicutes; Bacillus/Staphylococcus
NCBI_TaxID=1423;
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SIMILARITY: BELONGS TO THE ARCHAEAL
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0; Mismatches
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EMBL; AB006424; BAA33120.1; -.
EMBL; Z99105; CAB12017.1; -.
PIR; S47267; S47267.
SubtiList; BG10924; purT.
InterPro; IPR003135; ATP-grasp.
Pfam; PF02222; ATP-grasp; 1.
Purine biosynthesis; Transferase; M
CONFLICT 240 241 KH ->
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P14247;
01-JAN-1990
01-NOV-1995
15-DEC-1998
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[1]
SEQUENCE FROM N.A.
STRAIN=DSM 1224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _METVA
                                                                                                                                            SEQUENCE OF 171-386 FROM N.A.

STRAIN-DSM 1224;

MEDLINE-89362493; PubMed=2475640;

Lechner K., Heller G., Boeck A.;

"Organization and nucleotide sequence of a transcriptional unit of Methanococcus vannielii comprising genes for protein synthesis elongation factors and ribosomal proteins.";

J. Mol. Evol. 29:20-27(1989).

-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPT OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.

-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                          Palm P., A Submitted
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Methanococcus.
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(Rel. 32,
(Rel. 37,
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                                                                                                                     BELONGS
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to the EMBL/GenBank/DDBJ databases.
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Last sequence update)
Last annotation updat
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tute of Bio
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i -> ND (IN REF. 1).
5E3642CD6CAF90F7.CRC64;
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Mismatches
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                                                                                                                    POLYMERASE BETA' CHAIN FAMILY.
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(EC 2.7.7.6).
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                                                                    Multigene
ACT_SITE
SEQUENCE
                                                                                                          EMBL; U15947; AAC49030.1; -.
InterPro; IPR001099; Chal_stil_synt.
Pfam; PF00195; Chal_stil_syntC; 1.
Pfam; PF02797; Chal_stil_syntC; 1.
PROSITE; PS00441; CHALCONE_SYNTH; 1.
Flavonoid biosynthesis; Transferase;
                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=95241498; PubMed=7724563;
Durbin M.L., Learn G.H., Huttley G.A.,
"Evolution of the chalcone synthase ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ipomoea purpurea (Common morning glory).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X73293; CAA51729.1; -.
EMBL; X15970; CAA34086.1; -.
PIR; S06620; S06620.
InterPro; IPR002879; RNA_pol_A2.
Pfam; PF01854; RNA_pol_A2; 1.
Transferase; Transcription; DNA-directed RNA polymerase; SEQUENCE 386 AA; 42982 MW; 0D26292FB45BA6A7 CRC64;
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NCBI_TaxID=4121;
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                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: 3 malonyl-CoA + 4-coumarcyl-CoA = 4 CoA + naringenin-chalcone + 3 CO(2).

PATHWAY: PART OF THE BIOSYNTHETIC PATHWAY FOR ALL CLASSES OF FLAVONOIDS, A LARGE CLASS OF SECONDARY PLANT METABOLITES, MANY OF WHICH ARE BRIGHTLY COLORED.

SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                 :. Natl. Acad. Sci. U.S.A. 92:3338-3342(1995).
FUNCTION: THE PRIMARY PRODUCT OF THIS ENZYME IS 4,2',4',6'-
TETRAHYDROXYCHALCONE (ALSO TERMED NARINGENIN-CHALCONE OR CHALCONE)
WHICH CAN UNDER SPECIFIC CONDITIONS SPONTANEOUSLY ISOMERIZE INTO
                                                                                                                                                                                                                                                                                                                                                                                                                        NARINGENIN.
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7; Conserv
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33, Last sequence update)
41, Last annotation update)
B (EC 2.3.1.74) (Naringenin-chalcone
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                                                                     SIMILARITY.
352C478C1AF892B6
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gene family
                                                                                                               Acyltransferase;
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Best

Local Similarity

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                     SEQUENCE FROM N.A.

STRAIN=CV. PETITE HAVANA; TISSUE=Pistil
STRAIN=CV. PETITE HAVANA; TISSUE=Pistil
MEDLINE=93005740; PubMed=1392607;
Goldman M.H., Pezzotti M., Seurinck J.,
"Developmental expression of tobacco pi
novel extensin-like proteins.";
Plant Cell 4:1041-1051(1992).

-i- TISSUE SPECIFICITY: PISTIL (STIGMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
Odell C., Bowman S., B
Submitted (MAR-1995) t
                                                                                                                                                                                                                                                       EXLP_TO
Q03211;
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Q03694;
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                                                                                                                                       Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyt
Spermatophyta; Magnoliophyta; eudicot
Asteridae; euasterids I; Solanales; S
NCBI_TaxID-4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWI
between
                                                                                                                                                                                                     01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Pistil-specific extensin-like protein precursor (PELP).
                                                                                                                                                                                                                                                                                                                                                           1131 GTSSKKT
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SGD; S0004817; YMR204C.
Hypothetical protein.
SEQUENCE 420 AA; 47314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yei
Eukaryota; Fungi; Ascomycota; Saccha
Saccharomycetales; Saccharomycetacea
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01-NOV-1997 (Rel. 35, Last sec)
01-NOV-1997 (Rel. 35, Last and
Hypothetical 47.3 kDa protein
YMR204C OR YM8325.05C.
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               DEVELOPMENTAL
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AEITINI 203
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btyledons; core eudicots;
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S GRADUALLY INCREASE DURING
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Bank/DDBJ databases.
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                                                               7., Mariani C.;
pistil-specific genes encoding
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EMBL; Z14019; CAA78397.1; -.

PIR; JQ1696; JQ1696.

InterPro; IPR000419; Pollen_Ole_e_I; 1.

Structural protein; Signal; Repeat; C

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P12458;
01-OCT-1989
01-OCT-1989
15-JUL-1999
                                                                                                                                                                                Burland T.G., Paul E.C.A., Oetliker M., Dove W.F.;

"A gene encoding the major beta tubulin of the mitotic spindle in Physarum polycephalum plasmodia.";

Mol. Cell. Biol. 8:1275-1281(1988).

-!- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. I BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE BE CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN.

-!- FUNCTION: THIS IS THE MAJOR BETA TUBULIN OF MITOTIC SPINDLE.

-!- SUBUNIT: DIMER OF ALPHA AND BETA CHAINS.

-!- SUBCELLULAR LOCATION: MITOSIS IN THE SLIME MOLD PLASMODIUM DIFROM THE PROCESS IN MANY EUKARYOTES. THE TUBULIN CHAINS MUST TRANSPORTED TO THE NUCLEI FOR INTRANUCLEAR ASSEMBLY OF THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Physarum polycephalum 
Eukaryota; Mycetozoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-88216603;
                                                  between
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by non-
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DEVELOPMENTAL STAGE:
SIMILARITY: BELONGS
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SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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(Tubulin beta-major chain).
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Myxogastria;
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Pred. No. 72;
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Best Local
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J. Cell Sci. 105:903-911(1993).

-!- FUNCTION: TUBULIN IS THE MAJOR CONST BINDS TWO MOLES OF GTP, ONE AT AN EXCHAIN AND ONE AT A NONEXCHANGEABLE S

-!- SUBUNIT: DIMER OF ALPHA AND BETA CHA
-!- SIMILARITY: BELONGS TO THE TUBULIN F
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InterPro; IPR000217; Tubulir
InterPro; IPR003008; Tubulir
Pfam; PF00091; tubulin; 1.
PRINTS; PR01161; TUBULIN.
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P32256;

01-OCT-1993 (Rel.:

01-OCT-1993 (Rel.:

15-JUL-1999 (Rel.:
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or send a
PRINTS; PRO1161; TUBULIN.

PROSITE; PS00227; TUBULIN; 1.

PROSITE; PS00228; TUBULIN_B_AUTOREG;

Microtubules; GTP-binding.

NP_BIND 145 151 GTP (PO)
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PROSITE; PS00228; TUBULIN_B_AUTOREG;
Microtubules; GTP-binding; Multigene
NP_BIND 140 146 GTP (PO)
SEQUENCE 454 AA; 50364 MW; A913D4
                                                                  DictyDb; DD01044; tubB.
InterPro; IPR002453; Beta_tubulin.
InterPro; IPR000217; Tubulin.
InterPro; IPR003008; Tubulin_FtsZ.
Pfam; PF00091; tubulin; 1.
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Ennis H.L., Chisholm I
"The highly divergent
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Eukaryota; Mycetozoa; Dictyosteliida;
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A913D46AF63F1AD4 CRC64;
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  (POTENTIAL).
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A Palmiter R.D., Findley S.D.;

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30-MAY-2000 (Rel. 39
16-OCT-2001 (Rel. 40
Zinc transporter 1 (SLC30A1 OR ZNT1.
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SEQUENCE
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MGD; MGI:1345281; Slc30a1.
InterPro; IPR002524; Cation_efflux.
Pfam; PF01545; Cation_efflux; 1.
Zinc; Transport; Transmembrane; Multigene
CYTOPLASMIC (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for centities requires a license agreement (See http://www.isb-sib.ch/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                   TRANSMEM
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Pred. No. 77;
0; Mismatches
 POTENTIAL.

CYTOPLASMIC (POTENTIAL).

6 X 2 AA APPROXIMATE REPEATS

N-LINKED (GLCNAC. . .) (POTEN

7C4FF93FC13CDA22 CRC64;
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EXTRACELLULAR
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CYTOPLASMIC (POTENTIAL)
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Murinae; Mus
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Pfam; PF00479; G6PD; 1.

Pfam; PF002781; G6PD_C; 1.

PRINTS; PR00079; G6PDHDRGNASE.

PRODOm; PD001129; G6PD; 1.

PROSITE; PS00069; G6P_DEHYDROGENASE; 1

Oxidoreductase; NADP; Glucose metaboli

ACT_SITE 202 202

BY SIMILA.

SEQUENCE 507 AA; 58547 MW; C66F3FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gwinn M., Nelson W., DeBoy R., Kolonay Elsen J., Fraser C.M.;
"Genome sequences of Chlamydia trachoma pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
-!- CATALYTIC ACTIVITY: D-glucose 6-phc 1,5-lactone 6-phosphate + NADPH.
-!- PATHWAY: FIRST STEP IN PENTOSE PHOSE-!- SIMILARITY: BELONGS TO THE GLUCOSE-
ZNT1_RAT
Q62720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-MoPn / Nigg;

MEDLINE-20150255; PubMed-10684935;

Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,

Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,

White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,

White O., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,

Linher K., Weidman J., Khouri H., Craven B., McClarty G., Salzberg S.L.,
                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G6PD_CHI
Q9PKKB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydia muridarum.
Bacteria; Chlamydiales;
NCBI_TaxID-83560;
                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as modified and this statement is not reentities requires a license agreement or send an email to license@isb-sib.o
                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. between the Swiss Institute of Biointhe European Bioinformatics Institute
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16-OCT-2001 (Rel. 40, Last sequence of 16-OCT-2001 (Rel. 40, Last annotation Glucose-6-phosphate 1-dehydrogenase
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TC0457; -.
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Mismatches
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No. 84;
matches
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FE1562391A6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOSPHATE PATHWAY.
SE-6-PHOSPHATE DEHYDROGENASE
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(EC 1.1.1.49) (G6PD).
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                                                                                                                                                                                                                             lism; Complete proteome.
              507 AA:
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                                                                                                                                                                                                                   Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel.
30-MAY-2000 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                           Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Intestine; MEDLINE=98226729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE-Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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194
               56
                                      Local
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              NTSNSNG
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545; Cation_efflux; 1.
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                               Conservative
               62
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                                                                                                                                                                                                 Transmembrane; Multigene
10 CYTOPLASMIC (
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39,
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                                      0.6%;
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Last sequence up
Last annotation
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CYTOPLASMIC (POTENTIAL).

POTENTIAL.

EXTRACELLULAR (POTENTIAL)

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

6 x 2 AA APPROXIMATE REPE.

N-LINKED (GLCNAC. . . ) (POTENTIAL).
                           Score 7; UB 1
Pred. No. 84;
0; Mismatches
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CYTOPLASMIC
POTENTIAL.
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Murinae; Rat
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EMBL; PIR;

; M18264; A29605; ?

AAA26677.1; A29605.

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RESULT
SPA2_ST
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J. Mol. Biol. 272:573-590(1997).
-i- SUBCELLULAR LOCATION: Type I membran
-i- DOMAIN: THE N-TERMINAL HALF CONTAINS
WHILST THE C-TERMINAL HALF IS THE CE
-i- MISCELLANEOUS: IMPORTANT IMMUNODIAGN
ABILITY TO BIND THE FC FRAGMENT OF A
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MEDLINE-97467196;
Tashiro M., Tejero
Montelione G.T.;
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Bacteria; Firmi
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MEDLINE-88112878; PubMed-2828190;
MEDLINE-88112878; PubMed-2828190;
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Gouda H., Torigoe H., Saito A., Sato Particle and Structure staphylococcal protein A: comparisons
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"Structural studies on the four repet protein A from Staphylococcus aureus. Eur. J. Biochem. 78:471-490(1977).
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MEDLINE-97110349; PubMed-8952510;
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1-3.

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12 X 8 AA 2

2-1.

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2-11.
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K -> D (IN REF. 2).
E78C538D4B5E88F5
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                                                                                                                                                                                                                                                                                                                                                                                                            red. No. 84;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 508;
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        EMBL; V01287; CAA24596.1; -.

PIR; A03500; QVSAA.

PIR; A19498; A19498.

HSSP; P38507; 1BDD.

InterPro; IPR003132; B_domain.

InterPro; IPR002482; LysM.

Pfam; PF02216; B; 5.

Pfam; PF00746; Gram_pos_anchor; 1

Pfam; PF01476; LysM; 1.

SMART; SM00257; LysM; 1.

SMART; SM00257; LysM; 1.

SMART; SM00257; LysM; 1.

PROSITE; PS00343; GRAM_POS_ANCHOR IGG-binding protein; Repeat; Transignal 499 519

CHAIN 37 498 EXTR
TRANSMEM 499 519 POTE CHAIN 37 332 5X

REPEAT 37 100 1-1.

REPEAT 37 100 1-2.

REPEAT 37 303 340 2-1.

REPEAT 349 356 2-3.

REPEAT 349 356 2-3.

REPEAT 349 356 2-3.

REPEAT 349 356 2-3.

REPEAT 349 356 2-3.

REPEAT 365 372 2-6.

REPEAT 365 372 2-6.

REPEAT 389 396 2-8.

REPEAT 389 396 2-8.

REPEAT 381 388 2-7.

REPEAT 381 389 396 2-8.

REPEAT 397 404 2-9.

REPEAT 421 428 2-12
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J. Biol. Chem.
[2]
REVISIONS.
STRAIN=8325-4;
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Uhlen M., Chem. 7
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Lindberg M.;
"Complete sequence of
gene evolved through
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B_domain. Gram_pos_anchor. LysM.

ANCHORING

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Transme POTENTI.

mbrane; Cell wall; Signal.

IMMUNOGLOBULIN G BINDING PROTEIN A.
EXTRACELLULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
5 x 57 AA APPROXIMATE TANDEM REPEATS.
1-1.
1-2.
1-3.
1-4.
1-5.
1-5.
12 x 8 AA APPROXIMATE TANDEM REPEATS.
2-1.
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2-3.
2-4.
2-5.
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2-8.
2-9.
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2-12.

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SEQUENCE OF 1-186 E
STRAIN-8325-4;
MEDLINE-83143997; P
Loefdahl S., Guss E
"Gene for staphyloc
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                       MEDLINE-83143997; PubMed*6338496;
Loefdahl S., Guss B., Uhlen M., Philipson L., Lindberg M.;
"Gene for staphylococcal protein A.";
Proc. Natl. Acad. Sci. U.S.A. 80:697-701(1983).
-!- SUBCELLULAR LOCATION: Type I membrane protein. Cell wall.
-!- DOMAIN: THE N-TERMINAL HALF CONTAINS THE IG-BINDING REGION
WHILST THE C-TERMINAL HALF IS THE CELL-WALL-BINDING DOMAIN.
-!- MISCELLANEOUS: IMPORTANT IMMUNODIAGNOSTIC REAGENT BECAUSE OF ITS
ABILITY TO BIND THE FC FRAGMENT OF A WIDE RANGE OF MAMMALIAN
IMMUNOGLOBULINS.
-!- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS
IN THE REGION OF THE MEMBRANE ANCHOR.
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through multiple duplica
m. 259:1695-1702(1984)
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X MEDLINE-90175385; PubMed=2155425;

XA Kono T., Doi T., Yamada G., Hatakeyama M., Minamoto S., Tsudo M.,

XA Miyasaka M., Miyata T., Taniguchi T.;

XA Miyasaka M., Miyata T., Taniguchi T.;

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Best Local S
Matches 7
                                                                                                                                                   EMBL; M28052; AAA39283.1; -.
PIR; A35052; A35052.
HSSP; P14784; IILN.
MGD; MGI:96550; I12rb.
InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003531; Hematopo_receptor_S_F1.
Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 1.
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P16297;
01-AUG-1990
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SEQUENCE
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MOUSE
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SEQUENCE
  TRANSMEM
DOMAIN
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01-AUG-1990 (Rel. 15, Last sequence up
01-FEB-1995 (Rel. 31, Last annotation
Interleukin-2 receptor beta chain prec
(High affinity IL-2 receptor beta sub
                                                          CHAIN
DOMAIN
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Mammalia; Eutheria;
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institue modified and this statement entities requires a license
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                                                                                                                  Receptor;
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                                                                                                                                       PROSITE;
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us musculus (Mouse).
s musculus (Mouse).
charvota; Metazoa; Chordata; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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7; Conser
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Transmembrane;

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524 AA;
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                                                                                                                  HEMATOPO_REC_S_F1; 1.
brane; Glycoprotein;
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INTERLEUKIN-2 F
EXTRACELLULAR (
POTENTIAL,
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BY SIMILARITY,
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N -> D (IN REF. 3).
0A615C73C61316EF CRC64;
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Pred. No.
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precursor (IL-2 r
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                                                        RECEPTOR BETA CHAIN (POTENTIAL).
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//www.isb-sib.ch/announce,
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Murinae; Mus
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RESULT 46
C166_CARAU
ID C166_C
AC Q90304
DT 01-NOV
DT 30-MAY
DT 01-MAR
DE CD166
OS CATASS
OC EUKARY
OC ACTINC
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                                                                                                                                                                                                                                                                                                               Differentiation 56:21-29(1994).

-!- FUNCTION: CELL ADHESION MOLECULE. INVOLVED IN NEURITE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC INTERACTIONS.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- TISSUE SPECIFICITY: PRESENT ON ALL RETINAL GANGLION CELLS (RGCS) AND THEIR AXONS (IN EMBRYO). ABSENT FROM MATURE AXONS ALONG MOST OF THEIR LENGTH, BUT IS PRESENT ON NEW AND GROWING AXONS DERIVED FROM THE RGCS AT THE RETINAL MARGIN. REMAINS ON ADULT RGCS ONLY AT CELL-CELL CONTACT SITES AND IS CONTINUOUSLY FOUND IN THE RETINAL AXON TERMINAL ARBOR LAYERS OF THE ADULT TECTUM.

-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

-!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 EMBL; L25056; AAC38015.2; -. HSSP; Q13740; 1KJC. InterPro; IPR003006; Ig_MHC. InterPro; IPR003600; Ig_like InterPro; IPR003596; Ig_v.
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the fish retinotectal system wit
DM-GRASP/SC-1/BEN.";
                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It between the Swiss Institute of Bioinfo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laessing U., Giordano S., Stecher B., Lottspeich F., Stuermer C.A.O.; "Molecular characterization of fish neurolin: a growth-associated cell surface protein and member of the immunoglobulin superfamily in the fish retinotectal system with similarities to chick protein
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lano S., Stecher
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red. Usage by and for commercial
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X MEDLINE-94299040; PubMed-8026643;

X Laessing U., Giordano S., Stecher B., Lottspeich F., Stuermer C.A.O.;

A Laessing U., Giordano S., Stecher B., Lottspeich F., Stuermer C.A.O.;

T "Molecular characterization of fish neurolin: a growth-associated

T cell surface protein and member of the immunoglobulin superfamily in

T the fish retinotectal system with similarities to chick protein

T DM-GRASP/SC-1/BEN.";

Differentiation 56:21-29(1994).

C -!- FUNCTION: CELL ADHESION MOLECULE. INVOLVED IN NEURITE EXTENSION B

C -!- SUBCELLULAR LOCATION: Type I membrane protein.

C -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

C -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

-!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
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01-NOV-1997 (Rel. 35, I
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MEDLINE-94376084; PubMed-8089660;

MEDLINE-94376084; PubMed-8089660;

Kanki J.P., Chang S., Kuwada J.Y.;

"The molecular cloning and characterization DM-GRASP homologs in zebrafish and mouse.";

J. Neurobiol. 25:831-845(1994).
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Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Cypriniformes; Cyprinidae; Danio.
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FTE; PS00290; iG_
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llarity 100.0%;
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IG-LIKE V-TYPE DOMAIN 1.

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IG-LIKE C2-TYPE DOMAIN 3.
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Best Local S
Matches 7
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IL1R_HUMAN STANDARD;
P14778;
01-APR-1990 (Rel. 14, Cre
01-APR-1990 (Rel. 14, Las
01-MAR-2002 (Rel. 41, Las
Interleukin-1 receptor, t
(P80) (Antigen CD121a).
IL1R1 OR IL1RA OR IL1R.
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HSSP; Q13740; 1KJC.
ZFIN; ZDB-GENE-990415-30; cd166
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_WHC.
Interpro; IPR003596; Ig_WHC.
Interpro; IPR003596; Ig_V.
Pfam; PF00047; ig; 5.
SMART; SM00406; IG_MHC; 1.
PROSITE; PS00290; IG_MHC; 1.
Cell adhesion; Immunoglobulin derepeat; Signal.
SIGNAL 1 24 CD.
CHAIN 25 564 CM;
TRANSMEM 508 528 PO;
DOMAIN 31 117 IG
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CARBOHYD 465 465 V-I
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CARBOHYD 465 465 LFI
SEQUENCE 564 AA; 61273 MW; LFI
                                                                                                                                                                                                       Eukaryota; Metazoa; C
Mammalia; Eutheria; F
NCBI_TaxID=9606;
[1]
                                            Chua
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                                                                          SEQUENCE FROM N.A. TISSUE-Liver; MEDLINE-90098789;
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
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                                         A.O.,
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larity 100.0%;
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        CDNA
                                         PubMed=2532321;
U.;
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          type
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CD166 ANTIGEN HOMOLOGEXTRACELLULAR (POTENT POTENTIAL.

CYTOPLASMIC (POTENTIAL)

IG-LIKE V-TYPE DOMAIN

IG-LIKE C2-TYPE 
IG-LIKE C2-TYPE

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PKPG -> R (IN REF. 2).
7C293A607929 CRC54;
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                                                                                                                                                                                                                                                                                           ta; Vertebrata;
hini; Hominidae;
     !ibroblast type interleukin-1
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LULAR (POTENTIAL).
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Interpro; IPR003006; Ig_MHC.
Interpro; IPR003006; Ig_like.
Interpro; IPR004076; Intlk1_rece
Interpro; IPR004075; Intrlkn1_rece
Interpro; IPR004074; Intrlkn1_rece
Interpro; IPR004074; Intrlkn1_rece
Interpro; IPR004074; Intrlkn1_rece
Interpro; IPR000157; TIR.
IPR001582; TIR; 1.
PF101582; TIR; 1.
PRINTS; PF01582; INTRLEUKN1R1.
PRINTS; PR01536; INTRLEUKN1R1.
PRINTS; PR01537; INTRLKN1R12F.
SMART; SM00410; IG_like; 1.
SMART; SM00410; IG_like; 1.
PROSITE; PS50104; TIR; 1.
IMMUNOGlobulin domain; Transmemb
Repeat; 3D-structure.
SIGNAL 1 17
CHAIN 18 366
DOMAIN 337 356
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Nucleic Acids
[2]
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[4]
X-RAY C
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PIR; S
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MEDLINE-97215903; PubMed-9062193;
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March C.J., Dowe
"Cloning the int
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TISSUE-T-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L; X16896; CAA34773.1;
L; M27492; AAA59137.1;
; S06928; S06928.
; A36187; A36187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced ween the Swiss Institute of Bioinformatics European Bioinformatics Institute. There a by non-profit institutions as long as ified and this statement is not removed. Us
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11RA; 17-JUN-98.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Ig_MHC.
; Ig_like.
; Intlkl_receptorI_pre.
; Intrlknl_receptorI.
; IntrlknlreceptorI_II.
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"Transcriptional regulation of squalene epoxidase by sterols and inhibitors in HeLa cells.";
J. Biol. Chem. 271:8053-8056(1996).
-!- FUNCTION: CATALYZES THE FIRST OXYGENATION STEP IN STEROL BIOSYNTHESIS AND IS SUGGESTED TO BE ONE OF THE RATE-LIMITING ENZYMES IN THIS PATHWAY.
-!- CATALYTIC ACTIVITY: Squalene + AH(2) + O(2) - (5)-squalene-2, epoxide + A + H(2)O.
-!- COFACTOR: FAD.
-!- COFACTOR: FAD.
-!- SUBUNIT: MAY FORM A COMPLEX WITH SQUALENE SYNTHASE.
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Nagai M., Sakakibara
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MEDLINE=97223458; PubMed=9070279;
Senju S., Nishimura Y.;
Senju S., Nishimura Y.;
"Identification of human and mouse GP-1, a
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""" 231:360-364(
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Biochem. Biophys. Res. Commun. 231:360-364(1997).
-1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, THYMUS,
-1- SIMILARITY: BELONGS TO THE AGP1/GTPBP1 FAMILY O
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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Q97779 loxodonta a
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EMBL; U66497; AAB07497.1; -.
HSSP; P16471; 1BP3.
InterPro; IPR002996; CR1A.
InterPro; IPR003529; Hematopo_receptor_L_F2.
InterPro; IPR003531; Hematopo_receptor_S_F1.
InterPro; IPR003531; Hematopo_receptor_S_F1.
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1
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GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED
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EMBL; U66496; AAB07496.1; -.
HSSP; P16471; 1Bp3.
InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor
InterPro; IPR003531; Hematopo_receptor
InterPro; IPR003531; Hematopo_receptor
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
PROSITE; PS01353; HEMATOPO_REC_L_F2;
PROSITE; PS01355; HEMATOPO_REC_S_F1;
Receptor.
SEQUENCE 958 AA; 109392 MW; 3F659
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Eukaryota; Metazoa; Mammalia; Eutheria;
NCBI_TaxID=9606;
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QQIDANWNIQCWLKGDLKLFICYVESLFKNLFRNYNYKVHLLYVLPEVLEDSPLVPQKGS 180
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B.D., Solar G.P., Yuan
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Cloff1 J.A., Shafer A.W., Zupancic T.J., Smith-Platika D., Snodgrass H.R.;
Platika D., Snodgrass H.R.;
Novel B219/OB receptor isoforms: possible role hematopoiesis and reproduction.";
Nat. Med. 2:585-589(1996).
EMBL; U52914; AAC50511.1; -.
HSSP; P16471; 1BP3.
InterPro; IPR002996; CR1A.
InterPro; IPR003951; FN_III.
InterPro; IPR003529; Hematopo_receptor_L_F2.
InterPro; IPR003529; Hematopo_receptor_S_F1.
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
Signal; Receptor.
Signal; Receptor.
21 21 POTENTIAL.
CHAIN
22 896 B219/OB RECEPTOR I
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Q13594;
Q1-NOV-1996 (TrembLrel. O1, Created)
Q1-NOV-1996 (TrembLrel. O1, Last sequence update)
Q1-DEC-2001 (TrembLrel. 19, Last annotation update)
Q1-DEC-2001 (TrembLrel. 19, Last annotation update)
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Q1-DEC-2001 (TrembLrel. 19, Last sequence update)
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Q1-DEC-2001 (TrembLrel. 19, Last sequence update)
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                                                                                                                                                                                                                         y Match 58.5%; Local Similarity 99.9%; tes 781; Conservative
QPINMVKPDPPLGLHMEITDDGNLKISWSSPPLVPFPLQYQVKYSENSTTVIREADKIVS
QPINMVKPDPPLGLHMEITDDGNLKISWSSPPLVPFPLQYQVKYSENSTTVIREADKIVS
                                                                        GLYVIVPVIISSSILLLGTLLISHQRMKKLFWEDVPNPKNCSWAQGLNFQK
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B219/OB RECEPTOR ISOFORM HUB219
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L; Hominidae;
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[1]
SEQUENCE FROM
TISSUE-LIVER;
                   InterPro;
InterPro;
InterPro;
                                                                                                                  MEDLINE-96206286; PubMed-8616721; Cioffi J.A., Shafer A.W., Zupancic Platika D., Snodgrass H.R.;
                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
NCBI_TaxID=9606;
                                                                                                                                                                                                                                     Q13593 PRELIMINARY; PRT; 906 AA.
Q13593;
Q13593;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
B219/OB RECEPTOR ISOFORM HUB219.2 PRECURSOR.
                                                        hematopoiesis and reproduction.
Nat. Med. 2:585-589(1996).
EMBL; U52913; AAC50510.1; -..
HSSP; P16471; 1BP3.
                                                                                                      Platika D., Snodgrass H.R.;
"Novel B219/OB receptor isoforms:
          InterPro;
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FIIEWKNLNEDGEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFT 829
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LPDSVVKPLPPSSVKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVY
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ATSLLVDSILPGSSYEVQVRGKRLDGPGIWSI
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                                                                                                                                                                  FROM N.A.
         IPR002996; CR1A.
IPR003961; FN_III.
IPR003529; Hematopo_receptor_L_F2.
IPR003531; Hematopo_receptor_S_F1.
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Primates;
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Catarrh
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t; Hominidae: Homo.
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Matches 781; Conservative
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PROSITE; PS01353; HEMATOPO_REC_L_F2; UI
PROSITE; PS01355; HEMATOPO_REC_S_F1; UI
Signal; Receptor.

SIGNAL 1 21 POTENTIAL
CHAIN 22 906 B219/OB RI
SEQUENCE 906 AA; 103487 MW; 6D5112
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                                ODDIEKHO
                                                                                  FIIEWKNINEDGEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFT
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B219/OB RECEPTOR ISOFORM H
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
B219/OB RECEPTOR ISOFORM HUB219.1 PRECURSOR.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu Mammalia; Eutheria; Primates; Catarrhini; Hominidae; HUCBI_TaxID=9606;
[1]
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MEDLINE-96206286; PubMed-8616721;
Cioffi J.A., Shafer A.W., Zupancic T.J.
Platika D., Snodgrass H.R.;
Platika D., Snodgrass H.R.;
"Novel B219/OB receptor isoforms: possi
hematopoiesis and reproduction.";
Nat. Med. 2:585-589(1996).
EMBL; U52912; AAC50509.1; -.
HSSP; P16471; 1BP3.
InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor_
InterPro; IPR003531; Hematopo_receptor_
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
PROSITE; PS01353; HEMATOPO_REC_L_F2; UN
PROSITE; PS01353; HEMATOPO_REC_S_F1; UN
Signal; Receptor.
SIGNAL 1 21 POTENTIAL.
SIGNAL 1 21 POTENTIAL.
SEQUENCE 958 AA; 109419 MW; C7E0E81
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Local Similarity 99.9%;
hes 781; Conservative
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QPINMVKPDPPLGLHMEITDDGNLKISWSSPPL
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TFVSTVNSLVFQQIDANWNIQCWLKGDLKLFICYVESLFKNLFRNYNYKVHLLYVLPEVL 169
DAKSKSVSLPVPDLCAVYAVQVRCKRLDGL
                                                                                           LPDSVVKPLPPSSVKAEITINIGLLKISWEKPV
                                                                                                                                                                                          VYCCNEHECHHRYAELYVIDVNINISCETDGYLTKMTCRWSTSTIQSLAESTLQLRYHRS 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATSLLVDSILPGSSYEVQVRGKRLDGPGIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVS 349
ATSLLVDSILPGSSYEVQVRGKRLDGPGIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVS 349
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Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo
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B219/OB RECEPTOR ISOFORM HUB219.1.
; C7E0E8D18428677B CRC64;
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                         GYWSNWSNPAYTVVMDEKVPMRGPEFWRII 649
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r_S_F1.
   SNWSNPAYTVVMDIKVPMRGPEFWRII
                                                                                         FPENNLQFQIRYGLSGKEVQWKMYEVY 589
                                                                                                                                                                                        Smith-Gbur J., Mikhail A.,
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C TISSUE-ADIPOSE TISSUE;

A Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

R EMBL; AF225873; AAF35387.1; ~.

R HSSP; P16471; 1BP3.

R InterPro; IPR002996; CR1A.

R InterPro; IPR003961; FN_III.

R InterPro; IPR003961; FN_III.

R InterPro; IPR003529; Hematopo_receptor_L_F2.

R InterPro; IPR003531; Hematopo_receptor_S_F1.

R Pfam; PF00041; fn3; 2.

R PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.

R PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
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Matches 84
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SEQUENCE FROM N.A.
TISSUE-ADIPOSE TISSUE;
MEDLINE-98408931; PubMed-9738551;
Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen "Monkey leptin receptor mRNA: sequence, tissue distribution, expression in the adipose tissue of normal, hyperinsulinemic, 2 diabetic rhesus monkeys.";
Obes. Res. 6:353-360(1998).
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Q9MYL1;
Q9MYL1;
Q9MYL1;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
LEPTIN RECEPTOR SHORT ISOFORM.
Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
NCBI_TaxID-9544;
                                                                                                                                        Receptor.
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Pred. No.
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Matches 84
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SEQUENCE FROM N.A.

TISSUE-ADIPOSE TISSUE;

Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin Submitted (JAN-2000) to the EMBL/GenBank/DDBJ d EMBL; AF225875; AAF35389.1;

HSSP; P16471; 1BP3.

InterPro; IPR003961; FN_III.

InterPro; IPR003529; Hematopo_receptor_L_F2.

InterPro; IPR003529; Hematopo_receptor_S_F1.

InterPro; IPR003531; Hematopo_receptor_S_F1.

Pfam; PF00041; fn3; 2.

SMART; SM00060; FN3; 1.

PROSITE; PS01355; HEMATOPO_REC_L_F2; UNKNOWN_1.

PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.

Receptor.

SEQUENCE 925 AA; 105721 MW; EC09C27EC29C5F3
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Q9MYL2;
Q9MYL2;
Q1-OCT-2000 (TrEMBLrel. 15, C
Q1-OCT-2000 (TrEMBLrel. 15, I
Q1-DEC-2001 (TrEMBLrel. 19, I
LEPTIN RECEPTOR LONG FORM.
Mammalia; Eutheria; I
Cercopithecinae; Mac
NCBI_TaxID=9544;
[1]
SEQUENCE FROM N.A.
MEDLINE=98408931; Pul
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01-OCT-2000 (TrE)
01-OCT-2000 (TrE)
01-DEC-2001 (TrE)
LEPTIN RECEPTOR :
                                                                                                                            Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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MEDLINE-98408931; PubMed-9738551;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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Bank/DDBJ databases.
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SEQUENCE FROM N.A.

TISSUE-ADIPOSE TISSUE;

Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin Submitted (JAN-2000) to the EMBL/GenBank/DDBJ d EMBL; AF225874; AAF35388.1; -.

HSSP; P16471; 1BP3.

InterPro; IPR003996; CR1A.

InterPro; IPR003961; FN_III.

InterPro; IPR0039529; Hematopo_receptor_L_F2.

InterPro; IPR003529; Hematopo_receptor_S_F1.

Pfam; PF00041; fn3; 2.

SMART; SM00060; FN3; 1.

PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.

PROSITE; PS01355; HEMATOPO_REC_L_F2; UNKNOWN_1.
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Gustafson T.A., Ortmeyer H.K., Bodkin I Submitted (JAN-2000) to the EMBL/GenBar EMBL; AF222960; AAF34683.1; -.

HSSP; P16471; 1BP3.

InterPro; IPR002996; CR1A.

InterPro; IPR003961; FN_III.

InterPro; IPR003529; Hematopo_receptor_InterPro; IPR003529; Hematopo_receptor_InterPro; IPR003531; Hematopo_receptor_Pfam; PF00041; fn3; 2.

SMART; SM00060; FN3; 1.

PROSITE; PS01353; HEMATOPO_REC_L_F2; U1 PROSITE; PS01355; HEMATOPO_REC_S_F1; U1 Receptor.

SEQUENCE 1163 AA; 132295 MW; 6B7B89
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SEQUENCE FROM N.A.
TISSUE=ADIPOSE TISSUE;
MEDLINE=98408931; PubMed=9738551;
HOTTA K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen F.
"Monkey leptin receptor mRNA: sequence, tissue distribution, and the adipose tissue of normal, hyperinsulinemic, and hy
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Hematopo_receptor_L_F2.
Hematopo_receptor_S_F1.
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Best Local S
Matches 84
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HSSP; P16471; 1BP3.
InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo.
InterPro; IPR003531; Hematopo.
InterPro; IPR003531; Hematopo.
Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 2.
PROSITE; PS01353; HEMATOPO_RE;
PROSITE; PS01355; HEMATOPO_RE;
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01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor.
SEQUENCE
 Sus scrofa
Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
Mammalia; E
                             O02671 PRELIMINARY; PRT; 1
O02671;
O1-JUL-1997 (TrEMBLrel. 04, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequ
O1-JUN-2001 (TrEMBLrel. 17, Last annotation)
TRANSMEMBRANE LEPTIN RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OBR.
                     LEPR.
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01-OCT-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
TRANSMEMBRANE LEPTIN REC
                                                                                                                                                                                                                                                                                                                                                                                                 "Expression, Detection,
                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                      "Expression, (OBR) Gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
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SWPMSKVNIVQSLSAYPLNSSCVI
                                                                                                                                               TKPRGKFTYDAVYCCNEHECHHRYAELYVIDVNINISCETDGYLTKMTCRWST 451
                                                                                                                                      TKPRGKFTYDAVYCCNEHECHHRYAELYVIDVNINISCETDGYLTKMTCRWST 445
                                                                                                                                                                             4.5%;
Similarity 100.0%;
53; Conservative
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84; Conservative
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h; Metazoa;
Eutheria;
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          (Pig).
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                                                                                                                                                                                                                                                                   PN3; 2;
HEMATOPO_REC_L_F2;
HEMATOPO_REC_S_F1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Suina; Suidae; Sus.
 Chordata;
                                                                                                                                                                                                                                                                                                               CR1A.
FN_III.
Hematopo_receptor_L_F2.
Hematopo_receptor_S_F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECEPTOR (FRAGMENT).
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                                                                                                                                                                                                                                 MW;
                                                                                                                                                                                                                                                                                                                                                                                                  Partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ¥
                                                                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                              0;
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Pred. No. 3.7e-80;
); Mismatches 0;
                                                                                                                                                                            Score 53; DB 6; Length 848
Pred. No. 3.9e-47;
); Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            753
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  Craniata
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                                        sequence update)
annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                  Cloning of Porcine Leptin Receptor
                                                                                  1165 AA
                                                                                                                                                                                                                                                                        UNKNOWN_1.
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 Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1194;
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                                                                                Query Match
Best Local S
Matches 43
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Best Local S
Matches 53
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MEDLINE-9722487; PubMed-9069130;

Ernst C.W., Kapke P.A., Yerle M., Rothschild M.

"The leptin receptor gene (LEPR) maps to porcin

Mamm. Genome 8:226-226(1997).

EMBL; AF092422; AAC61766.1; -.

EMBL; U72070; AAC48707.1; -.

HSSP; P16471; 1BP3.

InterPro; IPR002996; CR1A.

InterPro; IPR003529; Hematopo_receptor_L_F2.

InterPro; IPR003529; Hematopo_receptor_S_F1.

Pfam; PF00041; fn3; 1.

SMART; SM00060; FN3; 2.

PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.

PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.

Transmembrane.

SEQUENCE 1165 AA; 132548 MW; 1BEB562FEA282F
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O97778;
O97778;
O1-MAY-1999 (TrEMBLrel. 10, COL-MAY-1999 (TrEMBLrel. 10, LEPTIN RECEPTOR (FRAGMENT).
LEPR.
                                                                                                                                                                                                           Receptor.
NON_TER
NON_TER
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                                                                                                                                                                                                                                                                  (Elephas maximus) and the Submitted (MAR-1997) to EMBL; U95048; AAD00769.1
                                                                                                                                                                                                                                                                                  Elavsky N.E., Ernst C.W., Messer L.A., Rothschild M.F.; "Identification of Sequence Tagged Sites in the Asian Elephant (Elephas maximus) and the African Elephant (Loxodonta africana)."; Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Elavsky N.E., Ernst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Men
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NCBI_TaxID=9823;
[1]
                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            Elephas maximus (Indian elephant).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Proboscidea; Elephantidae; Elephas
NCBI_TaxID=9783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murphy B.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-LIVER;
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    ω
AVYCCNEHECHHRYAELYVIDVNINISCETDGYLTKMTCRWST 451
                                                                                   43;
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Similarity 100.0%;
53; Conservative
                                                                                                       Similarity
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larity 100.0%;
Conservative
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Pred. No.
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                                                                                                     Score 43;
Pred. No.
                                                                                                                                                                                       667857030937BA26 CRC64;
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T.,
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5.2e-
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                                                                                                                          6
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                                                                                                                         Length 57;
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Best Local Similarity 100.0%;
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InterPro; IPR003531; Hematopo_receptor_S_F1.
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ce Tagged Sites in the Asian Elephant
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he EMBL/GenBank/DDBJ databases.
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Submitted (MAR-1996) to the EMBL/GenBank/DDBJ (EMBL; U53144; AAB03088.1; -.
HSSP; P16471; 1BP3.
InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor_L_F2.
InterPro; IPR003531; Hematopo_receptor_S_F1.
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
PROSITE; PS01355; HEMATOPO_REC_L_F2; UNKNOWN_1
PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1
                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, C
01-NOV-1996 (TrEMBLrel. 01, L
01-DEC-2001 (TrEMBLrel. 19, L
LEPTIN RECEPTOR LONG FORM (FR
Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Cetartiod
Bovidae; Caprinae; Ovis.
NCBI_TaxID-9940;
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Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Rodentia; S
NCBI_TaxID=10116;
[1]
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Q62960;
Q1-NOV-1996 (TrEM
01-NOV-1996 (TrEM
01-DEC-2001 (TrEM
LEPTIN RECEPTOR.
SEQUENCE FROM N.A.

TISSUE=HYPOTHALAMUS;
MEDLINE=97217693; PubMed=9063654;
Method C.J., Simmons J.M., Matteri R.L., Keisler D.H.;
"Leptin receptor mRNA is expressed in ewe anterior padipose tissues and is differentially expressed in hyregions of well-fed and feed-restricted ewes.";
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Q28604;
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SEQUENCE
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STRAIN=SPRAGUE-DAWLEY;
Wang M.-Y., Unger R.H.
"Characterization of l
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of le
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Cetartiodactyla; Ruminantia; Pecora;
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Pred. No. 2.8e-3
0; Mismatches
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Sciurognathi;
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thi; Muridae;
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Murinae; Rat
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     Sone M., Satoh F., Mouri T., Brenner B.
"Leptin receptor gene expression in rat submitted (SEP-2000) to the EMBL; AF304191; AAG22877
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SEQUENCE FROM N.A.
Pfister-Genskow M., Eggen A
Pubmitted (JUN-1996) to the
Submitted (JUN-1996) to the
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P79115;
01-MAY-1997
01-MAY-1997
01-DEC-2001
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NON_TER
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Mammalia; E
Bovidae; Bc
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NON_TER
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Q9ERI4;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
LEPTIN RECEPTOR OB-RA (FRAGMENT).
Receptor.
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EMBL; U
                                                                                                                                                                                    Rattus norvegicus (Rat),
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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NCBI_TaxID=9913;
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l Similarity 100.08;
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EMBL/GenBank/DDBJ databases.
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Pred. No. 1.7e-12;
D; Mismatches 0;
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                                                     zie H.S., Murakami O., Arihara Z.,
nner B.M., Ito S.;
in rat kidney.";
/GenBank/DDBJ datubases.
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Best Local Similarity 100.0%;
Matches 18; Conservative
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Q1-NOV-1999 (TrEMBLrel. 12, COL-NOV-1999 (TrEMBLrel. 12, LEPTIN RECEPTOR (FRAGMENT).
                                Bell G.I.;

"Rat leptin splice variant Ob-Re.";

"Rat leptin splice variant Ob-Re.";

"Submitted (JUN-1997) to the EMBL/GenBank/DDBJ d
EMBL; AF007819; AAB63202.1; -.

HSSP; P40189; 1BQU.

InterPro; IPR003529; Hematopo_receptor_L_F2.

PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1
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Eukaryota; Metazoa; C
Mammalia; Eutheria; C
NCBI_TaxID=9823;
[1]
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O1-JAN-1998 (TrEMBLrel. O5, Last of
O1-DEC-2001 (TrEMBLrel. 19, Last of
LEPTIN RECEPTOR OB-RE (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE-HYPOTHALAMUS;
Matteri R.L.;
                                                                                                                                                                                                                                                                                              Chien E.K., Hara
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Q9XSH3;
Q9XSH3;
Q1-NOV-1999 (TrEMBLrel. 12, C:
Q1-NOV-1999 (TrEMBLrel. 12, L:
Q1-NOV-1999 (TrEMBLrel. 12, L:
Q1-NOV-1999 (FRAGMENT).
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Q9IA32;
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CTEMBLrel. 15, Cre
O1-OCT-2000 (TrEMBLrel. 15, Las
O1-DEC-2001 (TrEMBLrel. 19, Las
O1-DEC-2001 (TREMBLREL. 19, Las
CEPTIN RECEPTOR (FRAGMENT).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; C
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SEQUENCE
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SEQUENCE FROM N.A.
MEDLINE-20539125; PubMed-11086550;
MEDLINE-20539125; Priedman-Ei
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                                                                                                                                                                                                                                                                                                                                                                Archosauria;
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                                                                                                                                                                                                                                                                                                                                                   Gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Dodds A.C., Whitley
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Eukaryota; Metazoa; Chordata; Craniat
Mammalia; Eutheria; Perissodactyla; E
NCBI_TaxID=9796;
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red. No. 2.6e-09;
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formes; Phasianidae; Phasianinae;
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Mol. Cell. Endocrinol. 162:95-106(2000).
EMBL; AF169827; AAF31355.1; -.
HSSP; P40189; 1BQU.
InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor_L_F Pfam; PF00041; fn3; 1.
PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNO Receptor
       Richards M.P., Poch S.M., Ash Submitted (NOV-2000) to the E EMBL; AF321982; AAG40323.1; -HSSP; P40189; 1BQU.
InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 4.
                                                                                                                                                 Q9DDK1;
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
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LEPTIN RECEPTOR.
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Gallus gallus
Eukaryota; Met
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SEQUENCE
                                                                                                                     Meleagris gallopavo
Eukaryota; Metazoa;
Archosauria; Aves; 1
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STRAIN=WHITE LEGHORN;
MEDLINE=20314392; PubMed=10854702;
Horev G., Einat P., Aharoni T., Es
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NCBI_TaxID=9031;
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                                                                                  TISSUE *BRAIN;
                                                                                                              NCBI_TaxID=9103;
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miliarity 100.0%;
Conservative 0
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Metazoa; Chordata;
a; Aves; Neognathae.
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Neognathae; Galliformes;
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he chicken leptin-receptor
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hes 0;
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Meleagrididae; Meleag
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Phasianidae; Phasiani
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Q9IBA7;
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
                                           Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9823;
[1]
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Q9N1F9;
01-OCT-2000 (Trem)
01-OCT-2000 (Trem)
01-OCT-2000 (Trem)
LEPTIN RECEPTOR (
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SEQUENCE
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SEQUENCE
      SEQUENCE FROM N.A.

STRAIN-BREED YORKSHIRE/MEISHAN;

Lacroix D.A., Gevry N.Y., Ruiz-

"Porcine leptin receptor intron
                                                                                                                                                                                                                                                                                                  InterPro; IPR003961; FN InterPro; IPR003529; He Pfam; PF00041; fn3; 1. SMART; SM00060; FN3; 2.
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Gallus gallus (Chicken)
Eukaryota; Metazoa; Cho
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EMBL; AB033383; BA
HSSP; P40189; 1BQU
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(SEP-1999) to t
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BAA94292.1; -.
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Neognathae;
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Cetartiodactyla; S
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FN_III.
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; Galliformes; Phasianidae; Phasianinae;
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Mismatches 0;
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                                                             ca; Vertebrata; Euteleostomi; Suina; Suidee; Sus.
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Z.T., Murphy 8.D.;
rtial.";
ank/DDBJ databases.
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Q9QWV5;
Q9QWV5;
Q1-MAY-2000 (TrEMBLrel. 13, Cr
Q1-MAY-2000 (TrEMBLrel. 13, La
Q1-JUN-2001 (TrEMBLrel. 17, La
LEPTIN RECEPTOR LONG ISOFORM R
LEPR.
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Q1-NOV-1996 (TrEMBLrel. 01, C
Q1-NOV-1996 (TrEMBLrel. 01, L
Q1-DEC-2001 (TrEMBLrel. 19, L
LEPTIN RECEPTOR (FRAGMENT).
                  STRAIN=129;
Banks A.S., Myers M.G.Jr.;
"Murine Leptin Receptor Genon
"Murine (OCT-1998) to the E
Submitted (OCT-1998) to the E
EMBL; AF098792; AAD13218.1; -
MGD; MGI:104993; Lepr.
                                                                                                                                                  Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
NCBI_TaxID=10090;
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Dyer C.J., Simmons J.M., Matteri R.L., Keisler
"Ovine partial leptin receptor cDNA.";
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ
EMBL; U63719; AAB51695.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Peo
Bovidae; Caprinae; Ovis.
                                                                                                                                  SEQUENCE FROM N.A.
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[1]
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AF184172; /
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Similarity 100.0%;
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Brown J.A., Chua S.C., Liu
"A spontaneous mutation in
in CD-1 outbred mice.";
Submitted (MAY-1999) to tl
EMBL; AF152957; AAD41084.
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Q9WV88;
01-NOV-1999
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Mammalia; Eutheria;
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TISSUE~HYPOTHALAMUS;
Matteri R.L., Carroll J.
Submitted (AUG-1996) to
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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LEPTIN RECEPTOR (FRAGMENT).
                                                                NCBI_TaxID=10090;
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MEDLINE=20450683; PubMed=10997877; Nagase T., Kikuno R., Nakayama M., Hiro "Prediction of the coding sequences of XVIII. The complete sequences of 100 no code for large proteins in vitro."; DNA Res. 7:273-281(2000).
EMBL; AB046850; BAB13456.1; -.
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KIAA1630 PROTEIN (
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"Bovine ovarian leptin receptor partial cDNA sequence and expression in response to stimuli.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; UB3512; AAB62399.1; -
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InterPro; IPR001017; E1_dh.
InterPro; IPR000360; Transketolase.
Pfam; PF00676; E1_dehydrog; 1.
Pfam; PF02779; transket_pyr; 1.
Hypothetical protein.
SEQUENCE 919 AA; 102969 MW; 9387.
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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Strausberg R.;
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TISSUE-KIDNEY, RENAL
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GLYCOPROTEIN (FRAGMENT).
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"5' Alternate splicing of lepside splicing of lepside splicing of lepside splicing of lepside splicing of lepside splicing of lepside splicing of lepside splicing splicin
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01-OCT-2000 (TrEMBLrel. 15, Las
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LEPTIN RECEPTOR (FRAGMENT).
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Rodentia; S
NCBI_TaxID=10116;
Zambon M.C., Stockton J
"Influenza and RSV.";
Submitted (MAY-2001) to
[2]
SEQUENCE FROM N.A.
STRAIN-A965C;
Stockton J.D.;
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Q9JHF4;
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LEPTIN RECEP
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NON_TER
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STRAIN-A965C;
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Viruses; ssRNA negative-strand
Paramyxoviridae; Pneumovirinae;
NCBI_TaxID=12814;
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STRAIN-SPRAGUE-DAWLEY;
Lindell K., Bennett P.A.,
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SEQUENCE FROM N.A.
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Viruses; ssRNA negative-strand
Paramyxoviridae; Pneumovirinae;
NCBI_TaxID=12814;
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   Zambon M.C
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SEQUENCE FROM N.A.
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Stockton J.D.;
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Zambon M.C., Stockton J
"Influenza and RSV.";
Submitted (MAY-2001) to
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O1-JAN-1999 (TrEMBLrel. 09, Created)
O1-JAN-1999 (TrEMBLrel. 09, Last sequence update)
O1-JAN-1999 (TrEMBLrel. 09, Last annotation update)
HYPOTHETICAL 14.7 KDA PROTEIN C22A12.02C IN CHROMOSOME
SPAC22A12.02C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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Submitted (MAR-2001) to the E

EMBL; AJ306572; CAC35518.1; -

HSSP; P29312; 1A40.

InterPro; IPR000308; 14-3-3.

Pfam; PF00244; 14-3-3; 1.

PRINTS; PR00305; 1433ZETA.

ProDom; PD000600; 14-3-3; 1.

SMART; SM00101; 14-3-3; 1.

PROSITE; PS00796; 1433_1; 1.
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01-JUN-2001
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14-3-3-LIKE
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STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE-21359325; PubMed-11466286;

Noelling J., Breton G., Omelchenko M.V., Makaro Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J Tatusov R.L., Sabathe F., Doucette-Stamm L., So Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the bacterium Clostridium acetobutylicum.";

J. Bacteriol. 183:4823-4838(2001).

EMBL; AE007685; AAK79733.1; -.
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Hypothet1cal protein; Complete
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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NCBI_TaxID=1488;
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XM. MEDLING-21332296; PubMed-11427726;

XM. She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

XM. Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

XM. De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

XM. Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

XM. Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

XM. Charlebois R.L., Doclittle W.F., Duguet M., Gaasterland T.,

XM. Charlebois R.L., Doclittle W.F., Duguet M., Gaasterland T.,

XM. Charlebois R.L., Boolittle W.F., Duguet M., Gaasterland T.,

XM. The complete genome of the crenarchaeon Sulfolobus solfataricus P2.*;

XM. The complete genome of the crenarchaeon Sulfolobus solfataricus P2.*;

XM. The complete genome of the sensen C.W., Van der Oost J.;

XM. THE PROC. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

XM. THE PROC. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

XM. THE PROC. 1PRO03265; Endonuclse_III_FCL.

XM. The PROO730; HH-GPD; 1.

XM. THE PROC. 1PRO03265; Endo_3c.

XM. THE PROC. 1PRO03563; HHH_1.

XMART: SM00478; ENDO3C; 1.

XMART: SM00278; HhH1; 1.

XM. SMART: SM00278; HhH1; 1.

XM. SMART: SM00278; HhH1; 1.

XM. SMART: SM00278; Lyase; Complete proteome.

XM. SEQUENCE 236 AA; 26843 MW; 6FF5[ADB280ECCD2 CRC54;
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Best Local s
Matches
SEQUENCE FROM N.A.
TISSUE=OLFACTORY EPITHELIUM;
Mezler M., Breer H.;
"Two classes of olfactory receptors: m
studies.";
Submitted (NOV-1999) to the EMBL/GenBa
EMBL; AJ250750; CAC00721.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPCRHODOPSN.
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Q918C4;
Q1-OCT-2000 (
Q1-OCT-2000 (
Q1-JUN-2001 (
Q1-JUN-2001 (
Q1FACTORY REC
XB238.
                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniat
Amphibia; Batrachia; Anura; Mesobatra
Xenopodinae; Xenopus.
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NCBI_TaxID=8355;
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01-MAY-1997 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
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similarity 100.0%;
8; Conservative
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    1. 03, Last sequence update)
    1. 18, Last annotation update)
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achia; Pipoidea; Pipidae;
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Submitted (NOV-1999) to the EMBL/GenBank/DEMBL; AJ250752; CAC00723.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNPROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Q1-OCT-2000 (TrEMBLrel. 15, C
Q1-OCT-2000 (TrEMBLrel. 15, I
Q1-JUN-2001 (TrEMBLrel. 17, I
Q1-ACTORY RECEPTOR CLASS I.
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Q919B2;
Q1-OCT-2000 (TrEMBLrel. 15, C
Q1-OCT-2000 (TrEMBLrel. 15, L
Q1-JUN-2001 (TrEMBLrel. 17, L
Q1-ACTORY RECEPTOR CLASS I.
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SEQUENCE
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SEQUENCE
                                                                                          Xenopus laevis (African clawed frog). Eukaryota; Metazoa; Chordata; Craniata; Amphibia; Batrachia; Anura; Mesobatrach; Xenopodinae; Xenopus. NCBI_TaxID=8355;
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  SEQUENCE FROM N.A.
TISSUE-OLFACTORY EPITHELIUM;
Mezler M., Breer H.;
"Two classes of olfactory re
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Similarity 100.0%;
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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ALIGNMENTS

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RESULT: 1 AAW24051 ID AAW24051 standard; Protein; 1165 AA. XX

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insulin resistance; hypercholesterolaemia;
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The patent discloses obese receptor (ObR) proteins and nucleic acids encoding them. ObR protein participates in the regulation of mammalian to body weight. The invention also relates to a method of identifying therapeutic compounds for the treatment of a body weight disorder. The method involves contacting a cell that expresses a mammalian ObR compound. The method is useful for identifying compounds which modulate ObR gene expression and a mammalian SOCS-1 protein with a test compound. The method is useful for identifying compounds which modulate ObR gene expression and gene product activity, which cap be used as the control body weight particularly as therapeutic agents for treating body weight disorders, including obesity, cachexia and anorexia. The present sequence is human ObR protein mutant (Y1141F).

Note: This sequence is not shown in the specification but is derived the wild-type human ObR protein shown in figure 3 of the capting of the capting obesity.
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     PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP
                                                                                                                       GSSYEVQVRGKRLDGPGIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCIYKKENKI
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modulator; drug; type II diabetes;
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           98US-0178691.
97US-0961809.
                               98WO-US22797
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; cancer; AIDS: agri
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                                                                                 or; tyrosine phosphatase 1D; PTP-1D; ity; hypertension;, heart disease; culture.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides a method for identifying modulators of binding of CC a phosphorylated leptin receptor with tyrosine phosphatase 1D PTP-1D). CC The method comprises: (a) contacting a tyrosine-985 phosphorylated leptin receptor or its phosphorylated fragment with protein PTP-1D or its CC fragment in the presence and absence of a candidate agent under CC conditions in which in the absence of the agent the binding of the CC phosphorylated leptin receptor or fragment with PTP-1D or its fragment CC can be detected; and (b) detecting the binding of the phosphorylated CC leptin receptor and PTP 1D; where an increase in binding detected in the CC presence of the agent, indicates that the agent indicates binding, and a decrease in binding in the presence of the agent indicates; that the agent is a binding inhibitor. Modulators of tyrosine-985-phosphorylated leptin CC receptor-dependent PTP-1D phosphorylation are useful as drugs in weight CC loss diet regimens. The drugs identified can regulate adiposity and fat content of animals, particularly in mammals. Disorders that can be treated by PTP-1D modulators include obesity and its associated diseases, ceg. hypertension, heart disease and type II diabetes, and weight loss associated with cancer and AIDS. Additionally the agents identified may contact the content of animals can be associated where body weight of domestic animals can be condulated.
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11-DEC-1995;
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22-JAN-1996;
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95US-0570142.
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96US-0599455.
96US-0638524.
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Query Match 82.7%;
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                       Bennett B,
Rodrigues N
                                                                                                                     Human; WSX receptor; variant 6.4; identification; purification; ligand; activator; antibody; agonist; proliferation; obesity; differentiation; anaemia; treatment; neoplasia; anteriosclerosis; Type II diabetes; polycystic ovarian disease; cardiovascular disease; osteoarthritis; dermatological disorder; hypertension; insulin resistance; hypercholesterolaemia; hypertriglyceridaemia; cancer; cholelithiasis.
       WPI; 1997-372864/34
N-PSDB; AAT85576.
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The present sequence is the human WSX receptor variant.6.4, which can be used to identify and purify ligands and activators. An anti-WSX receptor antibody can be used as an agonist to activate the WSX receptor, leading to enhanced proliferation or differentiation of a cell expressing the WSX receptor. It can also be used to decrease body weight and/or fat-depot weight and/or food intake in an obese mammal. WSX receptor ligands can be used to enhance proliferation or differentiation of lymphoid, myeloid or expthroid blood cell lineages. This is useful when a mammal, especially a human, is suffering from decreased blood cell levels, i.e. anaemia, caused by chemotherapy, radiation therapy or bone marrow transplantation therapy. It can also be used to repopulate blood cells in a mammal. The products can also be used to treat, e.g. neoplastic disorders, arteriosclerosis, Type II diabetes, polycystic ovarian disease, cardiovascular diseases, insulin resistance, hypercholesterolaemia, hypertrusion, insulin and cholelithiasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WSX receptor and related antibodies and products for diagnosis and therapy, e. haematopoiesis or for treating tumours
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The present sequence is the human WSX receptor variant 12.1, which can be used to identify and purify ligands and activators. An anti-WSX receptor antibody can be used as an agonist to activate was receptor, leading to enhanced proliferation or differentiation of a cell expressing the WSX receptor. It can also be used to decrease body weight and/or fat-depot weight and/or fintake in an obese mammal. WSX receptor ligands can be used to enhance proliferation or differentiation of lymphoid, myeloid or erythroid blood cell lineages. This is useful when a mammal, especially a human, is suffering from decreased blood cell level
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Rodrigues M
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N-PSDB; AAT85577.
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Ouery Match 76.5%;
Best Local Similarity 100.0%;
Matches 891; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           Fletcher
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                                                                                                                                                                                          represents
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96US-0582825
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                                                                                                                                                                                                                                                                                                 receptor(s) and relate
obesity, diabetes and
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                                                                                                                                                                                             obesity
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                                                            the variants shown in AAW34497-W34501. the biological properties of naturally. The OB receptor proteins and OB are used for the treatment of obesity, rels and high cholestorol levels. The reat an individual for weight loss or
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Local Similarity 100.0%; Pred. No. 0;
les 839; Conservative 0; Mismatches
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transduction; ce
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the mouse OB receptor (leptin receptor). A fusion protein comprising cc extracellular domain and the human IgG Fc domain has been cc constructed. The ability of the OB receptor signal peptide to cc direct secretion of the fusion protein in transfected HEK 293 cells cc was compared to the ability of the human TRL signal peptide (see CC AAY05696) to direct secretion of a similar construct. The results cc showed that the heterologous TRL signal elevated the amount of cc transfected cells approximately 10-fold. TRL is a novel member of the tumour necrosis factor receptor superfamily. The invention cc provides full-length human and murine TRL proteins (see AAY05695-97), TRL fusion proteins, antigenic peptides and anti-TRL antibodies, as well as TRL nucleic acids (see AAX25320-22), recombinant expression condulators of cellular signal transduction, cellular conduction, cellular system cells, and cells involved in insulin resistance or conductor tesponse.
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Best Local Similarity
Matches 815; Conser
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therapy; OB receptor; leptin receptor.
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26-SEP-1997;
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larity 100.0%;
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           Obesity protein disorders, e.g. lipid levels
Claim
                                                                            31-DEC-1996;
04-JAN-1996;
                                                                                                                                                                   Obesity receptor
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)B; AAT98534.
                                                                                                                                sapiens
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Page
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96US-0582825
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                 receptor(s) and related DNA obesity, diabetes and high (
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151pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4;
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anorexia; cac
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Human OB-R variant Form 3.
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Form 3; infertility.
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Also described is the use of labelled DNA probes based on the OB-R
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Best Local S
Matches 781
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N-PSDB;
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                 The present sequence was used in the development of a novel method for detecting a defective obese protein or leptin receptor (OB-R) in cells. Them method comprises contacting RNA extracted from a cell population (preferably an ovary, prostate, testis, sperm, ova, coligonucleotide derived from a portion of the human OB-R variant form 1, 2 or 3 cDNA, and detecting hybridisation. Forms 2 and 3 are cassociated with infertility, as they are unable to correctly transduce signals from leptin binding. The detection method can be used to diagnose infertility, or predisposition to infertility, while treatments that inhibit or down regulate the variants, gene therapy to replace them in homozygotes or direct activation of downstream signal transduction can be used to improve fertility.

Calso described is the use of labelled DNA probes based on the OB-R sequence to screen for other variants!
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Query Match Best Local Similarity Matches 781; Conserva

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                                                                                                                                                                ATSILVDSILPGSSYEVQVRGKRLDGPGIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVS
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                                                     standard;
             defective obese leptin receptor;
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                           Form
                                                     Protein;
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variant
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              receptor; Form 1; i
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infertility.
                  OB-R;
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                                                                                                                                                                                                                                                                                                                                                                                           The present sequence was used in the development of a novel method for detecting a defective obese protein or leptin receptor (OB-R) in cells. Them method comprises contacting RNA extracted from a cell population (preferably an ovary, prostate, testis, sperm, ova, colloqueleotide derived from a portion of the human OB-R variant colliquiation and detecting hybridisation. Forms 2 and 3 are consociated with infertility, as they are unable to correctly transduce signals from leptin binding. The detection method can be used to diagnose infertility, or predisposition to infertility, while treatments that inhibit or down regulate the variants, gene therapy to replace them in homozygotes or direct activation of downstream signal transduction can be used to improve fertility.

Also described is the use of labelled DNA probes based on the OB-R sequence to screen for other variants.
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Best Local Sim
Matches 781;
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N-PSDB; AAT95779.
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LPDSVVKPLPPSSVKAEITINIGLLKISWEK
                                                                                                                                                      TFVSTVNSLVFQQIDANWNIQCWLKGDLKLFICYVESLFKNLFRNYNYKVHLLYVLPEVL 169
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Similarity 99.9%;
31; Conservative
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sing variant rece
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RESULT 19
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N-PSDB; AAT89193.
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                  Detecting
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    defective leptin receptor by hybridisation assay of obesity with agent that inhibits the defective also screening for compounds that supplement lepti
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CC (OB-R). Its sequence was deduced from a contiguous cDNA (AAT89193) CC derived from overlapping clones isolated from a human foetal liver CC library. The sequence shows near identity to a published OB-R CC sequence in the extracellular domain, with the exception of 3 mmino CC acids, but there is extensive diversity in the intracellular CC detection of OB-R in cells comprises extraction of FNNA and testing CC this for hybridisation to an oligonucleotide (I) derived from the CC OB-R variant gene, especially from the region beyond nucleotide CC 2770. Also claimed are methods of: (I) treating obesity by CC administration of an agent that inhibits expression of the OB-R (CC variant gene; and (2) identification of a compound that can supplement activity of leptin by: (1) incubating cells expressing CC OB-R variant first with leptin and then with a test compound, and CC (ii) comparing activation signals between cells treated and not treated with the test compound. Inhibition/down regulation of the CC variant OB-R (found in obese people) improves response of cells to compour that required to the receptor gene can be used to treat obesity. Labelled CC in brobes based on the gene can be used to treat obesity. Labelled CC determining predisposition to obesity), while the OB-R gene can be used to express recombinant OB-R (optionally as fusion protein) and CC in standard hybridisation assays. The OB-R gene can be used to express recombinant ob-R (optionally as fusion protein) and CC causing loss of appetite and hypermetabolic activity. Cells careen for (ant)agonists of leptin/OB-R interaction, also to generate CC of the variant receptor.
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Sequence

Query Match Best Local S Matches 781

Match 58.5%; Local Similarity 99.9%; les 781; Conservative

Score 681 Pred. No. 0; Mismaț

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DB 18; Length 958;

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                                                                  469
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Claim

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Fig

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RESULT 2
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ID AAW1
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XX AAW1
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                 Detecting defective form of leptin receptor by probing cellular RI - with oligonucleotide derived from DNA of receptor variant, also treatment of obesity by inhibiting expression of variant receptor and screening for agents that increase leptin activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leptin receptor; diagnosis; human
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DB; AAT72649.
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Score Pred.

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cytoplasmic domain at the C-terminal end, suggesting alternative splicing of a common precursor mRNA. A claimed method for detection of OB-R in cells comprises extraction of: RNA and testing this for hybridisation to an oligonucleotide (1) derived from the OB-R variant gene, especially from the region beyond nucleotide 2770. Also claimed are methods of: (1) treating obesity by administration of an agent that inhibits expression of the OB-R variant gene; and (2) identification of a compound that can supplement activity of leptin by: (1) incubating cells expressing OB-R variant first with leptin and then with a test compound, and (i) comparing activation signals between cells treated and not treated with the test compound. Inhibition/down-regulation of the variant OB-R (found in obese people) improves response of cells to weight regulation by leptin. Replacing variant OB-R by gene therapy (in homozygous individuals) can be used to treat obesity. Labelled probes based on the gene can be used to treat other variant forms of the receptor gene or to detect the variant gene (e.g. for determining predisposition to obesity), while the OB-R gene can be used to express recombinant OB-R (optionally as fusion protein) and in standard hybridisation assays. The OB-R gene can also be used to engineered to express variant receptor are used in method (2) to screen for (ant)agonists of leptin/OB-R interaction, also to generate antibodies that competitively inhibit, neutralise or enhance activity of the variant receptor.
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Ųγ Ş Ş Ωy δõ Q 용 Вp 몽 В 밁 Ş 밁 Ş Query Match Best Local S Matches 781 350 290 290 230 230 110 Match 58.5%; Local Similarity 99.9%; les 781; Conservative TFVSTVNSLVFQQIDANWNIQCWLKGDLKLF ATSLLVDSILPGSSYEVQVRGKRLDGPGIWS LPDSVVKPLPPSSVKAEITINIGLLKISWEK FHCIYKKENKIVPSKEIVWWMNLAEKIPQSQ fhciykkenkivpskeivwmnlaekipqsq 0 ed. No. 0; Mismatches DWSTPRVFTTQUVITYFPPKILTSVGSNVS 349 PVFPENNLQFQ1RYGLSGKEVQWKMYEVY 589 QPIFLLSGYTMWIRINHSLGSLDSPPTCV 529 ydvvsdhvskvtfinlnetkprgkftyda YDVVSDHVSKVTFFNLNETKPRGKFTYDA 409 qpifllsgytmwirinhslgsldspptcv Indels 0 Gaps 469 469 289 589 289 409

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23-JAN-1996;
20-MAR-1996;
                                                                                    Barut BA,
Zupancic '
This protein comprises a novel human haematopoietin receptor, designated Hu-B1.219 form 1, that has been detected in brain cells and shown to bind to the obese gene product, leptin. Its sequence was deduced from cDNA clones (see AAT75172) isolated from a human
                                                                       WPI;
                                                                                                                                                                                                                                   Haematopoietin
human; cancer;
                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                             anaemia;
                                             Using leptin to a immunodeficiency,
                                                                                                                                               21-JAN-1997;
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                                 Claim
                                                                  N-PSDB;
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DB; AAT75172.
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96US-0589915.
96US-0618957.
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n or myeloid deficiency
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Best Local Similarity 99.9%;
Matches 781; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence in the extracellular domain (only 3 amino acid variatic but differ extensively in the intracellular domain (downstream funcleotide 2771). Hu-B1.219 is a marker for haematopoietic and endothelial progenitor cells, especially those cells capable of long-term repopulation. Hu-B1.219 nucleic acid sequences or binding agents for Hu-B1.219 protein can be used in claimed meth for identifying haematopoietic progenitor cells in a cell mixtur or tissue, and for detecting cancer. A claimed method for treat suffering from a cancer which expresses Hu-B1.219, to result in suppression of cancer growth. Leukaemia is a typical Hu-B1.219 expressing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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No.
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an be used in claimed methods
tor cells in a cell mixture
A claimed method for treating
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RESULT 2
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                                                                                                    Query Match 49.8%;
Best Local Similarity 99.7%;
Matches 780; Conservative
                                                                                                                                                                   A novel haematopoetin receptor (AAR88912), HuB1.219 Form 3 protein, is the product of a cDNA clone (AAT12913) isolated from a human foetal liver library. 2 Other forms of HuB1.219 (see AAR88910 and AAR88911) have also been identified. The Hu-B1.219 protein, or a portion of it, is pref. prepd. by culturing a host cell engineered to express HuB1.219 cDNA. The Hu-B1.219 protein (whether in sol. form or expressed on the cell surface and opt. as part of a fusion protein) is used to screen peptide libraries to identify ligands of Hu-B1.219.
                                                                                                                                                                                                                                                                                                              WPI; 199
N-PSDB;
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                                                                                                                                                  Sequence
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14-SEP-1994;
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DB; AAT12913.
QPINMVKPDPPLGLHMEITDDGNLKISWSSPPLVPFPLQYQVKYSENSTTVIREADKIVS
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                                                                                                                                                   898
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94US-0306231
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871..898
/label- Transmembra
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prenatal
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testing and
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cancer
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Homo
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leukaemia; diag
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 14-DEC-1994;
            30-AUG-1995;
                       21-MAR-1996
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            95WO-US10965
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871..898
/label= Transmembra
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                                                                                               Hu-B1.219 For
                                                                                                                                 908
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                                              domain
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14-SEP-1994;

94US-0306231

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Best Local
Matches 7
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                  A novel haematopoetin receptor (AAR88911), HuB1.219 Form 2 protein, is the product of a cDNA clone (AAT12912) isolated from a human foetal liver library. 2 Other forms of HuB1.219 (see AAR88910 and AAR88912) have also been identified. The Hu-B1.219 protein, or a portion of it, is pref. prepd. by culturing a host cell engineered to express HuB1.219 cDNA. The Hu-B1.219 protein (whether in sol. form or expressed on the cell surface and opt. as part of a fusion protein) is used to screen peptide libraries to identify ligands of Hu-B1.219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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DB; AAT12912.
                     NGDTMKKEKNVTLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKETFLWTEQA
                                                  FHCIYKKENKIVPSKEIVWWMNLAEKIPQSQYDVVSDHVSKVTFFNLNETKPRGKFTYDA
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RESULT 2
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AC AAR8
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XX
PD 21-)
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PF 30-1
PR 14-1
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Query Match 49.8%;
Best Local Similarity 99.7%;
Matches 780; Conservative
                                                                      protein)
of Hu-Bl.
                                                                           A novel haematopoetin receptor (AAR88910), HuBl 219 Form 1 protein, is the product of a cDNA clone (AAT12911) isolated from a human foetal liver library. 2 Other forms of HuBl 219 (see AAR88911 and AAR88912) have also been identified. The Hu-Bl 219 protein, or a portion of it, is pref. prepd. by culturing a host cell engineered to express HuBl 219 cDNA. The Hu-Bl 219 protein (whether in solform or expressed on the cell surface and opt. as part of a fusion protein) is used to screen peptide libraries to identify ligands of Hm-mi 210
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N-PSDB;
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14-SEP-1994;
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94US-0306231.
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Score 580; DB Pred. No. 0; 0; Mismatches
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Matches 668
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                                                                                                                                                                                                                                                                                                                                                                                The ob-receptor (OB-R), a member of the cytokine receptor family is transcribed in the hypothalamus and is involved in obesity. The replacement mutant has had amino acids 420-496 the second CK-F3 module in OB-R deleted and replaced by amino acids 500-632. The replacement mutant together with mutants lacking a functional first CK-F3 module or a functional intracellular domain can be used in assays for the detection of ligands, agonists, antagonists and ligand mimetics. The leptin agonists identified can be used in situations where leptin insufficiency causes obesity, diabetes or infertility. The leptin antagonists identified can be used in the treatment of anorexia and cachexia. The mutant receptor nucleic acids can also be used in gene therapy for weight control, e.g. for treating obesity or anorexia.
                                                                                                                                                                                                                                                                                                                                                                  Sequence
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for gene therapy
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RESULT 2
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The present sequence represents a new variant form of the human leptin receptor, OB-R (obesity receptor). The sequence of the variant OB-R differs structurally from a published human OB-R sequence (Tartaglia e al., 1995, Cell 83: 1263-1271). There are 3 amino acid substitutions i the extracellular domain and extensive diversity in the intracellular cytoplasmic domain, ie. the region encoded by the sequence downstream nucleotide 2770. A new method for detecting a defective OB-R in cells comprises (a) extracting RNA from a cell population; (b) contacting the RNA with an oligonucleotide derived from nucleotide residue 2770 and beyond of AAT74022; and (c) detecting hybridisation of the RNA with th oligonucleotide. A new method for treating obesity consists of
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N-PSDB;
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                                                                                                                                                                                                                                                                                    a variant form of human leptin of predisposition to obesity, as of the variant receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     numan leptin receptor; obesity triple helix; predisposition.
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sequence composition
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RESULT 2
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AAW14841;

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nes 774; Conser
                                                                                                                                                                                                                                                                                                                                   leptin.
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                                                                                                                                                                                                                          FHCIYKKENKIVPSKEIVWWMNLAEKIPQSQYDVVSDHVSKVTFFNLNETKPRGKFTYDA 409
                                                                                                                                                                                                                                               40.7%;
nilarity 99.6%;
Conservative
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Pred. No. (
                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                       biting expression of the OB-R
antisense molecules, ribozymes or
Also claimed is a method for
lementing the biological activity
                                                                                                             SHQRMKKLFWEDV2NPKNCSWAQG
                                                                  HHTSCNGTWSEDVGNHTKFTFLWTEQA
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                                                                                                                                                                         Human haemopoietin receptor NR2 (AAW14841) interacts with leptin, and can be used to develop (ant)agonists, therapeutics and diagnostic reagents based on ligand interaction. Its amino acid sequence was deduced from an isolated DNA molecule (AAT64442).

Crecombinant NR2 can also be used in a claimed method to identify ligands capable of interacting with a haemopoietin receptor, and soluble NR2 polypeptides can be used in the treatment of disease, injury or abnormality in the nervous system, cerebral palsy, trauma cliduced paralysis, vascular ischaemia associated with stroke, neuronal tumours, motor neurone disease, Parkinson's disease, funtington's disease, Alzheimer's disease, multiple sclerosis, peripheral neuropathies associated with diabetes, heavy metal or alcohol toxicity, renal failure and infectious diseases such as the treatment of diseases, rubella, measles, chicken pox, HIV or HTLV-1.
                                                                                                                 Matches
                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huntington's disease; Alzheimer's disease; multiple sclerosis; peripheral neuropathy; heavy metal; alcohol; toxicity; kidneyl failure; infectious disease; herpes; rubella; measles; chicken pox; HIV; HTLV-1; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-212896/19
N-PSDB; AAT64442.
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                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                          for treatment of autoimmune
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Ng A, Nicola
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human
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                                                                 QQIDANWNIQCWLKGDLKLFICYVESLFKNLFRNYNYKVHLLYVLPEVLEDSPLVPQKGS
                    sapiens
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                                                                                                              33.3%;
illarity 99.7%;
Conservative
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WA, Willsont;
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Pred. No. 0;
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protein
                                          New three-dimensional structural coordinate of a protein complex of leptin and its receptor binding domain, for identifying and designing leptin mutants with superior biological activity, or agonists and antagonists -
                                                                                                                                                                   Amino acid sequence
                                                                  WPI; 2001-565574/63.
                                                                                      (BIOM-) BIOMOLECULAR ENG RES
                                                                                                07-MAR-2000; 2000JP-0062404.
                                                                                                           05-MAR-2001;
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                                                                                                                                                                                                  AAG63999
                              Example
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                                                                                                                                          Homo sapiens.
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                                                                                                                                                    CRH-leptin receptor; co-ordinate data.
                                                                             Hiroike
                                                                                                                                                                                                  standard;
                             Page 676-677; 683pp;
                                                                                                           2001WO-JP01666
                                                                                                                                                                             (first
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The specification describes a three-coordinate of a complex formed from its receptor (CRH-leptin receptor) applicable in identifying, searching

a three-d

-dimensional (3D) structural
leptin and a hinding domain of
The 3D structural coordinate is
g, evaluating or designing leptin
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identifying, uperior biol

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Matches
            The ob-receptor (OB-R), a member of the cytokine receptor family is transcribed in the hypothalamus and is involved in obesity. The soluble secreted form of leptin binding domain is used in the scree of OB-R ligands. The leptin agonists identified can be used in situations where leptin insufficiency causes obesity, diabetes or infertility. The leptin antagonists identified can be used in the treatment of anorexia and cachexia. The OB-R mutant receptor nucle treatment of anorexia and cachexia.
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effect on
loss. The
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infertility. The leptin antagonists treatment of anorexia and cachexia. acids can also be used in gene therap treating obesity or anorexia.
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                                                                                                                                                                                                                                                                                          anorexia;
                                                                                                                                                                                                                                                                                                 ob-receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 18.3%;
Local Similarity 100.0%;
nes 213; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                          29
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                                                                                                                          mutant
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                                                                                      Fig
                                                                                                                                                                                                                                                                                                  hypothalamus;
                                                                                                                                                                              Q:
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for gene therapy
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    swine poultry, sheep. An antibody spectomeasure the presence of OB-R in a samp nucleic acid molecule encoding OB-R car OB-R polypeptide associated with obese measure its encoded RNA and protein in nucleic acid molecule can be used in as
                                                            The present sequence represents a lept The OB-R can be used to treat obesity, a treatment for diabetes, high blood por in cosmetic compositions for reducing used in agriculture to produce leaner.
                                                                                                                                         Leptin receptor, OB-R, polypeptide optionally in conjunction with treapressure and high cholesterol
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                    leptin receptor (OB-R) protein, OB-Re. Ity, optionally in conjunction with od pressure and high cholesterol, lucing body weight. It may also be near food animals, e.g. beef cattle, specific for OB-R can be used to sample, optionally in vivo, while the can be used to detect defects in the can be used to detect defects in the can be nearly in a protein all disorders.
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The present sequence represents a leptin receptor (OB-R) protein, OB-Ra. CIT The OB-R can be used to treat obesity, optionally in conjunction with CIC a treatment for diabetes, high blood pressure and high cholesterol, CIC or in cosmetic compositions for reducing body weight. It may also be CIC used in agriculture to produce leaner food animals, e.g. beef cattle, CIC swine poultry, sheep. An antibody specific for OB-R can be used to nucleic acid molecule encoding OB-R can be used to detect defects in the CIC OB-R polypeptide associated with obese phenotypes, or diagnostically to fucleic acid molecule can be used in gene therapy, or the antisense CIC nucleic acid molecule can be used to antagonise leptin activity. The nucleic acid molecule, or the antisense nucleic acid molecule, can be used to treat weight loss e.g. associated with AIDS, cancer or anorexia
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nucleic
used to
nervosa.
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N-PSDB; AAT75703.
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1.5e-34;
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r diabetes, high blood
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can be
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Query Match Best Local S Matches 42

3.6%; Similarity 100.0%; 42; Conservative

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Score 42 Pred. N 0; Misma

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Best Local S
Matches 42
                                                          This protein comprises isoform c' of the rat ob receptor. The obreceptor has numerous isoforms resulting from alternative splicing; a novel isoforms, designated f, g and c' are disclosed (see AAW34258-60). Isoform c' differs from the 1162-residue wild-type protein (see AAW34257) in that after Lys-889 there are only 3 amino acids. The c' isoform can be expressed in host cells, particularly E. coli, yeast or mammalian cells. It is used to identify specific binding ligands. Agonists, antagonists and ligand mimetics can be identified that are potentially useful in the study, prevention and
                     adaptation of the speci-
                       treatment of obesity.
(NB. the amino acid sequence of isoform c' was produced by adaptation of the wild-type ob receptor sequence provided in Fig 1
                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat
Sequence
                                                                                                                                                                                                 New isoform(s) of the Ob specific binding ligands,
                                                                                                                                                                                                                                                     Caskey
                                                                                                                                                                                                                                                                                                                                                                                                           Ob receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                         (MERI ) MERCK & CO INC.
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06-MAY-1996;
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nes 42; Conservative
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                                                                                                                                         protein comprises isoform c' of
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the obesity protein receptor of the invention. The gene sequence may be used for screening of warm animals (such as rats) for spontaneous mutations resulting in to ob protein receptor gene which leads to animals having an obese phenotype. These are useful in the study of mechanisms of obesidevelopment of anti-obesity drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Misc-difference
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RESULT 3
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ob protein receptor (phenotype. These are development of anti-
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Misc-difference
 20-JUN-1996;
08-JAN-1996;
                                                                                        WO9725425-A1
                                                                                                                                                                                                                                             Murine WSX receptor
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                                       07-JAN-1997;
                                                                                                                                        hypertension; insulin hypertriglyceridaemia;
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  96US-0667197
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RESULT 3
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Best Local S
Matches 42
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                                                            /label= ECD
/note= "extracellular
838..860
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/note= "transmembrane
861..894
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/note= "cytoplasmic
317..321
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23..837
                                                                                                                                Location/Qualifiers
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obesity; cachexia; 
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28-DEC-1995;
22-JAN-1996;
26-APR-1996;
         Culpepper
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Best Local S
Matches 42
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N-PSDB;
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27-NOV-1995;
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08-DEC-1995;
11-DEC-1995;
28-DEC-1996;
22-JAN-1996;
26-APR-1996;
03-SEP-1996;
28-MAY-1997;
                        The patent discloses obese receptor (ObR) proteins and nucleic acids encoding them. ObR protein participates in the regulation of mammalian body weight. The invention also relates to a method of identifying therapeutic compounds for the treatment of a body weight disorder. The method involves contacting a cell that expresses a mammalian ObR protein, a JAK2 protein and a mammalian SOCS-1 protein with a test compound. The method is useful for identifying compounds which modulate ObR gene expression and gene product activity, which can be used as agents to control body weight particularly as therapeutic agents for treating body weight disorders, including obesity, cachexia and anorexia. The present sequence is short form ObR protein from murine.
                                                                                                                                                                                                                                            Identifying compounds for treating anorexia or cachexia, comprises correceptor protein, JAK2 protein and
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Matches 42; Conser
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                                                                                                                                                                                                                                          This protein comprises isoform f of the rat ob receptor. The obreceptor has numerous isoforms resulting from alternative splicing; a novel isoforms, designated f, g and c' are disclosed (see AAW34258-60). Isoform f differs from the 1162-residue wild-type protein (see AAW34257) in that after Lys-889 there are only 6 amino acids. In the cDNA (see AAT93104), these codons are then followed k a stop codon. The f isoform can be expressed in host cells, particularly E. coli, yeast or mammalian cells. It is used to identify specific binding ligands. Agonists, antagonists and ligand mimetics can be identified that are potentially useful in the study, prevention and treatment of obesity.

(NB. the amino acid sequence of isoform f was produced by adapted to the study of the wild-type of the recent of obesity.
                                AAW22105;
           16-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                          New isoform(s) of the Ob (leptin) receptor - specific binding ligands, potentially useful and treatment of obesity
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06-MAY-1996;
                                                    AAW22105
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                                                                                                      specification).
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AAW34259 RESULT

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AAW34259

standard; Protein;

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S Disclosure; ray.

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The present sequence represents a leptim.

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The OB-R can be used to treat obesity, optionally in ....

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The OB-R can be used to treat obesity, optionally in ....

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The OB-R can be used to treat obesity, optionally in which cholesters.

CC

The OB-R can be used to treat obesity, optionally in which cholesters.

CC

CC

The OB-R can be used for reducing body weight. It may also be used in agriculture to produce leaner food animals, e.g. beef cattle, or swine poultry, sheep. An antibody specific for OB-R can be used to molecule encoding OB-R in a sample, optionally in vivo, while the nucleic acid molecule associated with obese phenotypes, or diagnostically to measure its encoded RNA and protein in nutritional disorders. The nucleic acid molecule can be used in gene therapy, or the antisense nucleic acid molecule can be used to antagonise leptin activity. The can be used to antagonise leptin activity. The can be used to antagonise leptin activity. The can be used to antagonise leptin activity. The can be used to antagonise leptin activity. The can be used to antagonise leptin activity. The can be used to antagonise leptin activity. The can be used to antagonise leptin activity. The can be used to antagonise leptin activity. The can be used to antagonise leptin activity. The can be used to antagonise leptin activity. The can be used to antagonise leptin activity. The can be used to antagonise leptin activity. The can be used to antagonise leptin activity. The can be used to antagonise leptin activity. The can be used to antagonise leptin activity.
Leptin receptor, OB-R, polypeptide optionally in conjunction with treapressure and high cholesterol
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16-JAN-1996;
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96US-0586594.
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                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                           receptor has numerous isoforms resulting from alternative splicing;

C 3 novel isoforms, designated f, g and c' are disclosed (see

C AAW34258-60). Isoform g is much shorter than the 1162-residue

C wild-type sequence (see AAW34257). 18 N-terminal amino acids are

C spliced to a large fragment of the wild-type molecule, beginning at

C Pro-166. The isoform then extends for the remainder of wild-type

C ob receptor molecule. Alternatively, it could contain another

C isoform variation, such as isoform a, b, c, d, e or f. The g

C isoform can be expressed in host cells, particularly E. coli, yeast

C or mammalian cells. It is used to identify specific binding

C identified that are potentially useful in the study, prevention and

C treatment of obesity.

C (NB. the amino acid sequence of isoform g was produced by

adaptation of the wild-type ob receptor sequence provided in Fig 1
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Best Local S
Matches 42
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06-MAY-1996;
                  24-MAY-1996;
06-MAY-1996;
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RESULT 4
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Best Local s
Matches 42
25-APR-1996;
22-FEB-1996;
22-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                             Ob rece fatty;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This protein sequence comprises wild-type (lean) rat ob receptor. The ob receptor has numerous isoforms resulting from alternative splicing; 3 novel isoforms, designated f, g and c' are disclosed (see AAW34258-60). These isoforms also apply to mouse and human ob receptors. The isoforms can be expressed in host cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isoform(s) of the Obspecific binding ligands, and treatment of obesity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-558993/51.
N-PSDB; AAT93103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             particularly E. coli, yeast or mammalidentify specific binding ligands. Againgting and mimetics can be identified that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
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                                                                                                                                                                   Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the study,
                                                           18-FEB-1997;
                                                                                         28-AUG-1997.
                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                    Peptide
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atty; fa mud
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; Protein; 1162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prevention and treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                               obesity;
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 96GB-0008473.
96US-0090405.
96US-0013969.
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/note= "6"
860..1162 |
/label= Cytoplasmic_dom
269
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1.28
/label- Sig_peptide
29..1162
                                                           97WO-US02397.
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839..860
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29..830
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Pred. No. 2.2e-34;
); Mismatches 0;
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RESULT 4
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AC AAW2
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DT 23-F
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COB Rat
XX
COB Rat
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COB Ratt
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FH Key
FT Pept
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Best Local S
Matches 42
                                                  Domain
                   Misc-difference
                                Domain
                                                              Domain
                                                                                                                     Ob receptor; obesity; leptin; fatty; fa mutation; therapy.
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 W09731015-A1
                                                                           Protein
                                                                                                          Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                obesity
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                                                                                        Peptide
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                                                                                                                                                                              AAW23398 standard;
                                                                                                                                                                                                                                                                     Sequence
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DB; AAT64962.
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                                                                                                                                                                                                                                                                     1162 AA;
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                  /label=
269
                                                  /label=
839..860
                               /label- Transmembrane_domain
/note- "6"
860..1162
                                                              /label=
29..830
                                                                           /label= 9
29..1162
                                                                                                                                        (wild-type).
                                                                                             Location/Qualifiers
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             "site
                                                        Extracellular_domain
                                                                    Mat_protein
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                         Cytoplasmic_doma
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                                                                                                                                                                              1162
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Pred. No.
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             of.
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             mutation in
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2.2e-34;
             fa
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| and treatmen
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             0B-R"
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RESULT 4
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Best Local Similarity 100.0%;
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This protein comprises rat wild-type (i.e. lean) ob receptor (OB-R). Its amino acid sequence was deduced from a cDNA sequence (see AAT64961) obtained by PCR amplifications. The sequence differs at only 1 position from the OB-R sequence from rats with a fatty (fa) mutation; the fa OB-R mutant receptor has proline at amino acid 269 rather than glutamine (see AAW23399). This is a result of an A to C transversion in the fa OB-R gene (see AAT64962). Every tissue examined in an fa/fa Zucker rat was homozygous for this mutation. The wild-type and mutant OB-R can be expressed in prokaryotic or eukaryotic host cells. They are useful in assays to identify putative ligands, which may be receptor agonists or antagonists or bind with little effect, and which may be useful in understanding obesity and for its prevention and treatment.
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22-FEB-1996;
22-MAR-1996;
                                                                                                                                                                                                                                                                                                                    Ob receptor; ObR; cytokine receptor; eating disorder; obesity; cachexia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat wild-type and mutant ob receptor identification of new ligands for pr
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N-PSDB; AAT64961.
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96US-0090405.
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                                                                                                                                                                                                                                                                                                                    signal transduction;
anorexia; bulimia; diagnosis;
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30 TO

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03-SEP-1996;
27-NOV-1995;
04-DEC-1995;
08-DEC-1995;
11-DEC-1995;
28-DEC-1995;
22-JAN-1996;
26-APR-1996;
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                                                                      27-NOV-1996;
                                                                                                                                                                                               Modified-site
     96US-0708123.
95US-0562663.
95US-0569485.
95US-0570142.
95US-0583153.
96US-0638524.
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/label= CD
/note= "cytoplasmic c
317..321
                                                                     96WO-US19128
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695
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686
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657
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345
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187
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98
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73
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/note= '
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726
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RESULT 45
AAY13473
ID AAY13473
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated products obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 199
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The murine long form Ob receptor (ObR) (AAW19115) is a novel polypeptide that participates in the control of body weight and which is involved in signal transduction triggered by the binding of its natural ligand, Ob (leptin). It is a member of the class I cytokine receptor family and is predominantly expressed in the hypothalamus. Its amino acid sequence was deduced from a hypothalamus cDNA clone (AAT69591). A short form (AAW19114) of murine ObR, expressed in the choroid plexus, is associated with the obese phenotype in db/db mice. The 2 forms differ in the length of the cytoplasmic domain. ObR proteins, peptides, antibodies, agonists and antagonists can be used in the diagnosis and treatment of body weight disorders such as obesity, cachexia and anorexia.
                                        WPI; 199
N-PSDB;
                                                                                                                                                                                                                Mus
                                                                                                                                                                                                                                   Leptin; phosphorylated leptin receptor modulator; drug; weight loss; adiposit type II diabetes; cancer; AIDS: agricu
                   Identifying
                                                                                                                                                                      14-MAY-1999
                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                        AAY13473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PHARM
                                                                                           (UYRQ ) UNIV
                                                                                                                 26-0CT-1998;
31-0CT-1997;
                                                                                                                                                 27-OCT-1998;
                                                                                                                                                                                          WO9923493-A1
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                                                                                                                                                                                                               musculus.
                                        1999-327025/27
DB; AAX55587.
                                                                                                                                                                                                                                                                                                                                                                                                 1997-310525/28
                                                                                                                                                                                                                                                                                                                                                                                                                                          3.6%;
Similarity 100.0%;
42; Conservative
                                                                                                                                                                                                                                                                              Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT69591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ob receptor genes a for diagnosis or tacachexia, anorexia
                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1162
                    modulators
                                                                                                                                                                                                                                                                              ID No:
                                                                                            ROCKEFELLER.
                                                                                                                                                                                                                                                                                                   (first
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                                                                                                                 98US-0178691.
97US-0961809.
                                                                                                                                                 98WO-US22797.
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                                                                                                                                                                                                                                                                              N
                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                              of WO9923493
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                    agents
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treatment of b
ia and bulimia
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Pred. No
                    that
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                     mod
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                                                                                                                                                                                                                                   '. tyrosine phosphatase 1D; PTP-1D;
y; hypertension;, heart disease;
lture.
                     ulate leptin activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tide(s)
                                                                                                                                                                                                                                                                                                                                                                                                            SVVKPLPPS 541
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 18; L. 2.2e-34; 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ide(s) - useful to develop body weight disorders, e.g.
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Disclosure;

Page

67-74;

96pp;

English

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RESULT 46
AAE12615
ID AAE126
XX AAE126
XX AAE126
XX O3-JAN
XX Murine
XX Murine
XX Murine
XX Mus s
FH Key
FT Pepti
FT Prote
FT Domai
FT Domai
FT Domai
FT Domai
FT Domai
FT AX
PD 11-SE
XX
PR 29-AE
XX
PR 04-DE
PR 04-DE
PR 28-DE
PR 28-DE
PR 28-DE
PR 28-DE
PR 28-DE
PR 28-DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides a method for identifying modulators of binding of a phosphorylated leptin receptor with tyrosine phosphatase ID PTP-ID). The method comprises: (a) contacting a tyrosine-985 phosphorylated leptin receptor or its phosphorylated fragment with protein PTP-ID or its fragment in the presence and absence of a candidate agent under conditions in which in the absence of the agent the binding of the phosphorylated leptin receptor or fragment with PTP-ID or its fragment can be detected; and (b) detecting the binding of the phosphorylated leptin receptor and PTP ID; where an increase in binding detected in the presence of the agent, indicates that the agent enhances binding, and a decrease in binding in the presence of the agent indicates that the agent receptor-dependent PTP-ID phosphorylation are useful as drugs in weight content of animals, particularly in mammals. Disorders that can be treated by PTP-ID modulators include obesity and its associated diseases, e.g. hypertension, heart disease and type II diabetes, and weight loss associated with cancer and AIDS. Additionally the agents identified may condulated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 42
 27-NOV-1995;
04-DEC-1995;
'08-DEC-1995;
11-DEC-1995;
28-DEC-1995;
22-JAM-1996;
                                                                                                                                                                                                                                                                                                                                                                                  Murine; c
therapy;
                                                                                                    29-APR-1998;
                                                                                                                                                           US6287782-B1.
                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE12615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 3.6%;
Similarity 100.0%;
42; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                  obese receptor;
; obesity; cache;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
95US-0562663.
95US-0566622.
95US-0569485.
95US-0570142.
95US-0583153.
96US-0599455.
                                                                                                   98US-0069781
                                                                                                                                                                                                                                                                                 1..22
/label- 9
23..1162
                                                                                                                                                                                                                              /label=
838..860
                                                                                                                                                                                                  /label= Transmembrane_domain 861..1162
                                                                                                                                                                                                                                                         /label= Murine_mature_short_form_ObR_protein
23..837
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            ဌ
                                                                                                                                                                                                                                                                                                                                                                                      cachexia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein; 1162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                            receptor
                                                                                                                                                                                                                              860
                                                                                                                                                                                                                                                                                                                                                                                                 ObR;
                                                                                                                                                                                                                                          Extracellular_domain
                                                                                                                                                                                                                                                                                                Signal_peptide
                                                                                                                                                                                    Cytoplasmic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     b; Score 42; DB
b; Pred. No. 2.2
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      anorexia
                                                                                                                                                                                                                                                                                                                                                                                                 anorectic;
                                                                                                                                                                                                                                                                                                                                                                                                                           (ObR)
                                                                                                                                                                                                                                                                                                                                                                                                                           protein.
                                                                                                                                                                                                                                                                                                                                                                                               anabolic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 20; : 2.2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
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                                                                                                                                                                                                                                                                                                                                                                                                 pody
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                                                                                                                                                                                                                                                                                                                                                                                                  disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The patent discloses obese encoding them. ObR protein participates body weight. The invention also relates therapeutic compounds for the treatment The method involves contacting a cell t protein, a JAK2 protein and a mammalian compound. The method is useful for iden ObR gene expression and gene product ac agents to control body weight particulate treating body weight disorders, including the protein sequence is murine long form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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03-SEP-1996;
28-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anorexia receptor compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 20
N-PSDB;
                                   20-JUN-1996;
08-JAN-1996;
                                                                                                                                              Mus
                                                                                                                                                                   Type II diabetes; polycystic ovarian cardiovascular disease; osteoarthrit; hypertension; insulin resistance; hyphypertriglyceridaemia; cancer; cholel
                                                                                                                                                                                                       Murine; WSX receptor; mouse; identification; activator; antibody; agonist differentiation; anaemia; treatment; Type II diabetes; polycystic ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying compounds i anorexia or cachexia, creceptor protein, JAK2
                                                                                                                                                                                                                                                                                                                                          AAW24054 standard;
                                                                       07-JAN-1997;
                                                                                                                      WO9725425-Al.
                                                                                                                                                                                                                                                                                           17-MAR-1998
                                                                                                                                                                                                                                                                                                                   AAW24054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                47
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DB; AAD20541.
                                                                                                                                                                                                                                                                   WSX receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Similarity 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein,
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                                                                                                                                                                                                                                                                                          (first
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96US-0708123.
97US-0864564.
                                   96US-0667197
96US-0585005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tepper
                                                                       97WO-US00325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6;
                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109pp;
                                                                                                                                                                                                                                                                   extracellular
                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for treating body weight disorder, e.g. obesity, comprises contacting cell expressing mammalian Ob protein and mammalian SOCS-1 protein with test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Culpepper
                                                                                                                                                                                                                                                                                                                                          783
                                                                                                                                                                                                                               identifi
agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42
Pred. N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ceptor (ObR) proteins and nucleic acids rticipates in the regulation of mammalian so relates to a method of identifying treatment of a body weight disorder. g a cell that expresses a mammalian ObR mammalian SOCS-1 protein with a test 1 for identifying compounds which modulate product activity, which can be used as particularly as therapeutic agents for s, including obesity, cachexia and anorexia.
                                                                                                                                                                                                                                                                                                                                          ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ore 42; DB 22;
led. No. 2.2e-34;
Mismatches 0;
                                                                                                                                                                                                                                                                   dor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  form ObR protein.
                                                                                                                                                                                                                  ication; purification;
; proliferation; obesity;
neoplasia; arteriosclerosis;
                                                                                                                                                                                                                                                                   main.
                                                                                                                                                                       lithiasis.
                                                                                                                                                                                 percholesterolaemia;
                                                                                                                                                                                                         disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JA,
                                                                                                                                                                                             dermatological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    White DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the murine WSX receptor extracellular domain, which can be used to identify and purify ligands and cativators. An anti-WSX receptor antibody can be used as an agonist to activate the WSX receptor, leading to enhanced proliferation or differentiation of a cell expressing the WSX receptor. It can also be used to decrease body weight and/or fat-depot weight and/or food intake in an obese mammal. WSX receptor ligands can be used to enhance proliferation or differentiation of lymphoid, myeloid or expecially a human, is suffering from decreased blood cell levels, i.e. anaemia, caused by chemotherapy, radiation therapy or bone marrow transplantation therapy. It can also be used to repopulate blood cells in a mammal. The products can also be used to treat, e.g. neoplastic disorders, arteriosclerosis, Type II diabetes, polycystic ovarian disease, cardiovascular diseases, insulin creasistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 33
                                                                                                                                                                                                          Haematopoietic g
CR domain; CRD;
IL-5 receptor; a
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Rodrigues 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WSX receptor and related antibodies and products for diagnosis and therapy, e.g. haematopoiesis or for treating tumours
                                                                                                                                                                                                                                                                                                                                     AAB48723
            D'Andrea
                                                                                   01-MAY-2000;
                                                                                                                                                             Homo
                                                                                                                                                                                Haematopoietic growth factor receptor; cytokine receptor; subunit; CR domain; CRD; CRD3; h-beta-c subunit; GM-CSF receptor; IL-3 recepto IL-5 receptor; agonist; antagonist; myeloid leukaemia; cancer; human; lymphocyte leukaemia; non-haemopoietic tumour; inflammatory disease; asthma; rheumatoid arthritis; atherosclerosis; CR module; CRM; E-F lo
                                                                                                                                                                                                                                                                                     09-MAR-2001
                                                                                                                                                                                                                                                                                                            AAB48723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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and cholelithiasis.
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                                   (MEDV-) MEDVET
                                                            29-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                 1997-372864/34.
DB; AAT85578.
                                                                                                                                                             sapiens
                                                                                                                                                                                                                                                             leptin
                                                                                                                                                                                                                                                                                                                                                                                                                                                2.8%; Score 33;
Similarity 100.0%; Pred. No.
33; Conservative 0; Mismatci
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                                                                                                                                                                                                                                                             receptor
           Bagley
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            Vadas
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Matches 25
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08-MAR-1996;
22-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                            AAW32073
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                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                    non-insulin
                                                                                                                                                                                                                                                            Human; leptin;
                                                                                                                                                                                                                                                                                   Leptin internalisation sequence
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            1997-457487/42
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l Similarity 100.0%;
25; Conservative
                                                          RECEPTRON
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                                    Olsson
                                                                                  970S-0788820.
960S-0612999.
960S-0701382.
                                                                                                                                                                                                                                                            receptor;
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peptide;

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Mismatches

Score :

DB 22; 4.2e-1

Lenyth 25; Indels

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entry)

receptor fragment.

diabetes

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reatment; NIDDM;

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ACC XXX ACC XX

97WO-US03549

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CC The invention relates to a novel agonist or antagonist of a haemopoletic CC growth factor which is capable of binding a region of the CRD3 (cytokine ceceptor domain 3) of the human GM-CSF receptor/IL-3R/IL-5R shared CC subunit h-beta-c, or an equivalent CRD in a different haemopoletic CC growth factor receptor or other cytokine receptor. Binding of the CC agonist or antagonist has an effect on the interaction between CDR3 and CC CDR4 (or analogous domains) which mediates the agonist or antagonist property. In particular, the agonist or antagonist  The agonists are used for treating conditions currently cor antagonist. The agonists are used for treating conditions currently corrected by GM-CSF (granulocyte macrophage-colony stimulating factor), CC IL-3 (interleukin-3), IL-5, and other members of the family of the aemopoletic growth factors. Haemopoletic growth factor antagonists are cureful for treating diseases such as myeloid and lymphocyte leukaemias, conditions (e.g., asthma, rheumatoid arthritis and atherosclerosis). CC cytokine receptor subunits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New agonists or antagonists of haemopoletic growth factors for treating myeloid and lymphocyte leukemias, tumors and acute and chronic inflammation such as asthma, rheumatoid arthritis and atherosclerosis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 surface receptor, where the oligopeptide enhances the effect of ligand binding to the receptor expressed by a cell. The oligopeptide and cell can be used to screen for bioactive agents capable of modulating the internalisation of a cell surface receptor. Internalisation sequences of the extracellular domains of receptor inhibit internalisation of the receptor, but do not affect binding of the ligand. Inhibition of receptor internalisation results in more receptors at the cell surface to bind the ligand, i.e. an increase in ligand binding effectiveness. The increase in ligand signalling is useful for treating diseases where hormone sensitivity is reduced, e.g. non-insulin dependent diabetes
This sequence represents a peptide derived from the extracellular activation sequence of the human leptin receptor.

Activation sequences are involved in modulation of receptor
                                                                                                                      Claim 8;
                                                                                                                                                                                                          Modulating
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                                                                                                                                                                                                                                                                                                                                                                                      (RECE-) RECEPTRON INC
                                                                                                                                                                                                                                                                                                                                                                                                                                              24-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human leptin receptor-derived activation peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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                                                                                                                  Page 17; 92pp; English
                                                                                                                                                                                obesity
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                                                                                                                                                                                                          type-2
                                                                                                                                                                                                        cell
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4.9e-16;
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cc responses and are separate from the ligand binding site. Activation cc sequences are important in two distinct ways: in the modulation of cc receptor internalisation; and/or in the modulation of activation of the receptor. Use of peptides corresponding to the activation sequence of a creceptor can retard or inhibit receptor internalisation, thereby cc increasing or stabilising the steady-state number of active receptors on the cell surface. This has the effect of increasing signalling per unit cc for ligand. In addition, the receptor is classed as a type 2 cell surface receptor, meaning that such peptides can actually replace the requirement cc for the ligand, causing ligand-independent activation. This activation is consequent activation that occurs when two receptors bind one peptide subsequent activation that occurs when two receptors bind one ligand. This peptide could be used to treat disorders involving an inadequate or inappropriate response from its corresponding receptor e.g., obesity.

So Sequence 23 AA;
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Search completed: May 18, 2002, 07:03:58 Job time: 532 sec

Page 39

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GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpeper, Janice A.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF F
TITLE OF INVENTION: OBESITY AND CACHEXIA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
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TELEX: 200154
INFORMATION FOR SE
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APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C
STREET: 225 Franklin Street
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TELEPHONE: 617-542-5070
TELEPAX: 617-542-8906
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REFERENCE/DOCKET NUMBER: 07334/014001
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; APPLICANT: Tartaglia, Louis A.; APPLICANT: Tepper, Robert I.; APPLICANT: Culpepper, Janice A.; TITLE OF INVENTION: THE OB RECEPTOR AND TITLE OF INVENTION: DIAGNOSIS AND TREATITLE OF INVENTION: OBESITY AND CACHEX
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Matches 1165; Conservative
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ATTORNEY/AGENT INFORMATION:
NAME: Melklejohn, Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/016001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-8906
TELEFAX: 617-542-8906
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SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,153A
FILING DATE: 28-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
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CORRESPONDENCE ADDRE
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Pred. No. 0;
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ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Bl
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Ml
COMPUTER: IBM PC compatible
                                                                                     APPLICANT: Matthews, Wi
APPLICANT: Bennett, Bri
TITLE OF INVENTION: WSX
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
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KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMMPTTVVSILSTTDLEKGSVCISDQFN 960
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           floppy disk
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REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P098
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEFAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: Amino Acid
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Best Local Similarity 100.0%;
Matches 1165; Conservative (
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SOFTWARE: WinPatin (Genent
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 08-Jan-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
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TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINS
           TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
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Pred. No. 0;
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STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/638,524B
FILING DATE: 26-APR-1996
PRIOR APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/569,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/566,622
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APPLICANT:
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TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS:
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KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMMPTTVVSLLSTTDLEKGSVCISDQFN 960
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Culpepper, Janice A.
Hite, David W.
INVENTION: THE OB RECEPTOR A
INVENTION: DIAGNOSIS AND TRE
INVENTION: CACHEXIA
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225 Franklin Street
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Tepper, Robert
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TOPOLOGY: unknown
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IS-08-638-524B-4
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Best L
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ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/018001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-8906
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
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LENGTH: 1165 amino acids
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LENGTH: 1165 amino TYPE: Amino Acid TOPOLOGY: Linear :-667-197-2
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LENGTH: 1165 amino acids
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KDSFSNSSWEIEAQAFFILSDQHPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIYYL
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Pred. No. 0;
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; MOLECULE TYPE: ; FRAGMENT TYPE: US-08-708-123D-4
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US-08-708-123D-4
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino ---
TYPE: amin-
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APPLICANT: Tartaglia, Louis A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: White, David w.
TITLE OF INVENTION: THE OB RECEPTOR AFTITLE OF INVENTION: THE DIAGNOSIS AND TITLE OF INVENTION: INCLUDING OBESITY NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Versic
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/708,123D
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/58,524
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/59,455
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/583,153
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meikleichn, Ph.D., Apita L.
                                                                                                                                                           REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
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CITY: Boston
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Culpepper, Janice A.
White, David W.
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                                                                                                                     GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED GASVANFNLTESWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED
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KDSFSNSSWEIEAQAFFILSDQHPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIYYL
                  PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV
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US-08-779-457-
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667197
FILING DATE: 06/20/96
PRÍOR APPLICATION DATA:
APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986P:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEFAX: 415/952-9881
TELEFAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
                                                                                                                                           Query Match
Best Local Similarity
Matches 1165; Conserv
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APPLICANT: Kyung, Jin Kim
APPLICANT: Matthews, William
APPLICANT: Rodrigues, Maria L.
TITLE OF INVENTION: WSX RECEPTOR AC
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb f
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,45
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                  TYPE:
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Pred. No. 0;
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                                             GLYVIVPVIISSSILLLGTLLISHQRMKKLFWEDVPNPKNCSWAQGLNFQKPETFEHLFI
GLYVIVPVIISSSILLLGTLLISHQRMKKLFWEDVPNPKNCSWAQGLNFQKPETFEHLFI
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TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
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   YMPQFQTCSTQTHKIMENKMCDLTV
              YMPQFQTCSTQTHKIMENKMCDLTV
                                                                                         KDSFSNSSWEIEAQAFFILSDQHPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIYYL KDSFSNSSWEIEAQAFFILSDQHPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIYYL
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US-08-780-562-2

; Sequence 2, Application US/08780562

; GENERAL INFORMATION:
; APPLICANT: Matthews, William
; APPLICANT: Bennett, Brian
; TITLE OF INVENTION: WSX RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: Am:
; TOPOLOGY:
US-08-780-562-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: 94080

COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb flog
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,562
FILING DATE: 01/08/97
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/
FILING DATE: 01/08/97
PRIOR APPLICATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEFAX: 415/952-9881
TELEPHONE: 415/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1165; Conservative 0
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TYPE: Amino Acid
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Pred. No. 0;
); Mismatches
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APPLICANT: Tartaglia, Louine APPLICANT: Tepper, Robert I.
APPLICANT: Culpeper, Janice A.
APPLICANT: White, David W.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
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                                                                                                                      Sequence 4, Application US/09094410 GENERAL INFORMATION:
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TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
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                                                                                                                                                                                                              GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFAS
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NAME: Meiklejohn, Ph.D., Anita L
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEPHAX: 617-542-8906
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: un
MOLECULE TYPE:
FRAGMENT TYPE:
S-09-094-410-4
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1165; Conservative 0;
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APPLICATION NUMBER: 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/569,662
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Methletchn Ph.D. Apita I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/094,41
FILING DATE: 09-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/864,564
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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COUNTRY: US
7TD: 02110-2804
7TADABLE F
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GSSYEVQVRGKRLDGPGIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCIYKKENKI 360
                                    LGLHMEITDDGNLKISWSSPPLVPFPLQYQVKYSENSTTVIREADKIVSATSLLVDSILP 300
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Pred. No. 0;
Mismatches
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RESULT 10
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                                                                                Sequence 4, Application US/09137132 GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPT
TITLE OF INVENTION: THE DIAGNOSIS
TITLE OF INVENTION: INCLUDING OBE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
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          THE OB RECEPTOR AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF BODY INCLUDING OBESITY AND CACHEXIA: 50
                              WEIGHT
                               DISORDERS
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TOPOLOGY: unknown

MOLECULE TYPE: protein

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Best Local Similarity
Matches 1165; Conservat
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APPLICATION NUMBER: US/09/137,132
FILING DATE: 18-AUG-1998
PRIOR APPLICATION NUMBER: 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: 08/538,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
APPLICATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/01900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FO
MEDIUM TYPE: Disk
COMPUTER: IBM Comp
OPERATING SYSTEM:
SOFTWARE: FastSEQ
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              241
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STREET: 225 F
CITY: Boston
STATE: MA
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LGLHMEITDDGNLKISWSSPPLVPFPLQYQVKYSENSTTVIREADKIVSATSLLVDSILP 300
                                        NGHYETAVEPKFNSSGTHFSNLSKTTFHCCF
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larity 100.0%;
Conservative 0
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Franklin Street
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Diskette
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Pred.
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No. 0;
matches
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RESULT 11
US-09-950-149-4
; Sequence 4, Application US/09950149
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis;
                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VPSKEIVWWMNLAEKIPQSQYDVVSDHVSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH
                                                                                                                                                                                 GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFAS
                                                                                                                                                                                                                                                                                                    KDSFSNSSWEIEAQAFFILSDQHPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIYYL KDSFSNSSWEIEAQAFFILSDQHPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIYYL
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TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
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                    읁
                     INVENTION:
Culpepper, Janice A. White, David W. INVENTION: THE OB RECEPTED THE DIAGNOST
                                                             Tartaglia, Louis
Tepper, Robert I
       OB RECEPTOR AND DIAGNOSIS AND THE
                                                                            >
      ND METHODS
TREATMENT
      FOR J
      BODY
       WEIGHT
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      DISORDERS
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Best Local Similarity
Matches 1165; Conserv
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TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/069,781
FILING DATE: <UNKnown>
APPLICATION NUMBER: US 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: US 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: US 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: US 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: US 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: US 08/569,485
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07,334/08200
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSEQ for Windows Versic

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/950,149

FILING DATE: 10-Sep-2001

PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Ric
STREET: 225 Franklin
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                                             QQIDANWNIQCWLKGDLKLFICYVESLFKNLFR
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; APPLICANT: WELCHER, A
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TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
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                                                                                                  KDSFSNSSWEIEAQAFFILSDQHPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIYYL KDSFSNSSWEIEAQAFFILSDQHPNIISPHLTFSEGLDELLKLEGNFPEENNDKKSIYYL
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APPLICANT: FLETCHER, FREDERICK A.
TITLE OF INVENTION: OB PROTEIN RECEPTY
TITLE OF INVENTION: COMPOSITIONS AND PROTEIN RECEPTY
TITLE OF SEQUENCES:
33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION NUMBER: US/08/774,414
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol M.
REFERENCE/DOCKET NUMBER: A-382-A
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1216 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-774-414-7
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No. 0;
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                                                                                                                              RSEQDRNCSLCADNISGKTFVSTVNSLVF 120
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WIRINHSLGSLDSPPTCVLPDSVVKPLPP
                    WIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/671,049
FILING DATE: 27-Sep-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/774,414
FILING DATE: 31-DEC-1996
                                                                               ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                             NUMBER OF SEQUE
CORRESPONDENCE
                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                        GLYVIVPVIISSSILLLGTLLISHQRMKKLFWEDVPNPKNCSWAQGLNFQKPETFEHLFI
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                                                                                                                                                                                                                                                                                     GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFAS
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                                                                                                      COUNTRY: US
ZIP: 91320
                                                                                                                      ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland
CITY: Thousand Oaks
STATE: California
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FLETCHER, FREDERICK A.
INVENTION: OB PROTEIN RECEPTOR AND RELATED
COMPOSITIONS AND METHODS
                                                                                                                                                           SEQUENCES: 3:
DENCE ADDRESS:
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Local Similarity 100.0%;
les 1165; Conservative 0;
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NAME: Pessin, Karol M.
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GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYI
                                       GASVANFNLTFSWPMSKVNIVQSLSAYPLNSS(
                                                                                                                                                                 SSVKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV
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LENGTH: 1216 amino a
                                                                                                                                      PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGFEIWRIINGDTMKKEKNV
                                                                                                                           PDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTV
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER:
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                                         CVIVSWILSPSDYKLMYFIIEWKNLNED
                                                  CVIVSWILSPSDYKLMYFIIEWKNLNED
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US-OB-191-16
US-OB-199-974C-56
Sequence 56, Application US/08599974C
GENERAL INFORMATION:
APPLICANT: Friedman, Jeffrey M.
APPLICANT: Lee, GWO-Hua
APPLICANT: Lee, GWO-Hua
APPLICANT: Proenca, Ricardo
ITILE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC
ITILE OF INVENTION: ACIDS ENCODING THE RECEPTOR, AND USES THEREOF
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floopy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: EMP CCOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-OS
SOFTWARE: PC-DOS/MS-OS
SOFTWARE: PAPLICATION NUMBER: US/OB/599,974C
FILING DATE: 14-FEB-1996
CLASSIFICATION: 435
APPLICATION NUMBER: US 08/586,594
FILING DATE: 16-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-162 CP1
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
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US-08-599-974C-56
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Query Match 91.3%;
Best Local Similarity 99.9%;
Matches 1164; Conservative
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                         KHTASVTCGPLLLEPETISEDISVDTSWKNK
                                                         GLYVIVPVIISSSILLLGTLLISHQRMKKLFY
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FQMVHCNCSVHECCECLVPVPTAKLNDTLLM
                                                 GLYVIVPVIISSSILLLGTLLISHQRMKKLF
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SYNFSEAEGTEVTYEDESQRQPFVKYATLIS
                KHTASVTCGPLLLEPETISEDISVDTSWKNK
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               DEMMPTTVVSLLSTTDLEKGSVCISDQFN
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NSKPSETGEEQGLINSSVTKCFSSKNSPL
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                                                                                                                                                    NAME: Poissant, Brian M.
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 0089
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEPAX: 650-493-5556
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                  Query Match
Best Local S
Matches 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08713296 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  SOFTWARE: FASTSEQ Version 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/7
FILING DATE: 13-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatibl
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: METHODS FOR USING THE OBESE TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO TITLE OF INVENTION: DEVELOPMENT NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pennie & E
STREET: 1155 Avenue c
CITY: New York
STATE: NY
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                                 Local Similarity 99.0 nes 1164; Conservative
                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
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Mikhail, Adel A.
Barut, Bruce A.
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Pred. No. 0;
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TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEFAX: 133521
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
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GENERAL INFORMATION:
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Best Local Similarity 99.9%;
Matches 1164; Conservative
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STRANDEDNESS: sinc
TOPOLOGY: linear
MOLECULE TYPE: prote
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TITLE OF INVENTION: METHODS OF IDENTIFYING AGENTS
TITLE OF INVENTION: MODULATE LEPTIN ACTIVITY
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NO ORIGINAL SOURCE: ORGANISM: HOM
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Li, Cai
APPLICANT: Friedman, Jeffrey M.
TITLE OF INVENTION: METHODS OF IDENT
TITLE OF INVENTION: ACTIVITY
FILE REFERENCE: 600-1-205 N
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CURRENT FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
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LENGTH: 1165
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                        GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA
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nilarity 99.9%;
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; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Homo :
US-09-700-813-10
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APPLICANT: SIERRA-HONIGMANN, ROCIO
FITTLE OF INVENTION: MODULATION OF ANGIOGENE
FILE REFERENCE: 044574-5029
CURRENT APPLICATION NUMBER: US/09/700/813
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: PCT/US99/11209
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: US 60/086,354
PRIOR FILING DATE: 1998-05-28
UNMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.0
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Best Local Similarity 99.9%;
Matches 1164; Conservative
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Sequence 10, A
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                                                                         FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCL
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 GSSYEVQVRGKRLDGPGIWSDWSTPRVFTTQD
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RESULT 19
US-09-948-933-256
; Sequence 256, Application US/09948933
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES AS:
TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AN:
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL000787
; CURRENT APPLICATION NUMBER: US/09/948,933
; CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/231,399
PRIOR FILING DATE: 2000-09-08
; MUMBER OF SEQ ID NOS: 6404
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 256
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TYPE: PRT
ORGANISM: Human
|S-09-948-933-256
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Local Similarity
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99.9%;
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        DEMMPTTVVSLLSTTDLEKGSVCISDQFN 960
                               WEDVPNPKNCSWAQGLNFQKPETFEHLFI
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  EMMPTTVVSLLSTTDLEKGSVCISDQFN
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Sequence 73, Application US/09948947; GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GE
TITLE OF INVENTION: WITH TYPE II DIABETES AN
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000786
CURRENT APPLICATION NUMBER: US/09/948,947
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 2172
SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 1165
TYPE: PRT
ORGANISM: Human
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                                                                                            otch 91.3%;
bal Similarity 99.9%;
1164; Conservative
                                                         GSSYEVQVRGKRLDGPGIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCIYKKENKI
  RYAELYVIDVNINISCETDGYLTKMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIH
                              VPSKEIVWWMNLAEKIPQSQYDVVSDHVSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH
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US-10-095-929-11
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; GENERAL INFORMATION:
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CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FOR
MEDIUM TYPE: Dis
                                                        NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie
STREET: 1155 Avenu
                                                                                                               TITLE
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                                                       Avenue
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GLYVIVPVIISSSILLLGTLLISHQRMKKLFWEDVPNPKNCSWAQGLNFQKPETFEHLFI 900 | GLYVIVPVIISSSILLLGTLLISHQRMKKLFWEDVPNPKNCSWAQGLNFQKPETFEHLFI 900 | GLYVIVPVIISSSILLLGTLLISHQRMKKLFWEDVPNPKNCSWAQGLNFQKPETFEHLFI 900
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                                                                                                                                                                                                                                                                                            Application US/10095929
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Shafer, Alan Wayne
FORM:
Diskette
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                                                                                                                                                              DEVELOPMENT
                                                                                                                                                                                                                     Thomas Joel
                                                                                            Edmonds LLP
of The Americas
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TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: 9
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Best Local
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
STRANDEDNESS: single
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FILING DATE: 12-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/618,957
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 008907-0033-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1050-493-4935
TELECOMMUNICATION: 650-493-4935
TELECOMMUNICATION: 650-493-556
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SSVKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV
                                                                                                                                                  GSSYEVQVRGKRLDGPGIWSDWSTPRVETTQDVIYFPPKILTSVGSNVSFHCIYKKENKI
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Similarity 99.9%;
64; Conservative
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Pred. No. 0;
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                                             APPLICANT: Tepper, Robert I.
APPLICANT: Culpeper, Janice A.
TITLE OF INVENTION: THE OB RECEPTOR ANI
TITLE OF INVENTION: DIAGNOSIS AND TREAT
TITLE OF INVENTION: INCLUDING OBESITY AND TREAT
TITLE OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,153
FILING DATE: 28-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
NAME: CORUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78!
TELECOMMUNICATION INFORMATION:
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TELEPHONE:
TELEFAX: 661
TELEX: 661

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MOLECULE TYPE:
S-08-583-153-4
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GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED
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RESULT 23
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       TELEFAX: 617-54.
TELEFAX: 617-54.
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
SEQUENCE: 1165 amino acids
                                                     PRIOR APPLICATION NUMBER: 08/583,153

APPLICATION NUMBER: 08/570,142

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: 08/570,142

FILING DATE: 11-DEC-1995

APPLICATION NUMBER: 08/566,622

FILING DATE: 04-DEC-1995

APPLICATION NUMBER: 08/562,663

FILING DATE: 11-NOV-1995

APPLICATION NUMBER: 08/562,663

FILING DATE: 11-NOV-1995

ATTORNEY/AGENT INFORMATION:

NAME: Meiklejohn, Ph.D., Anita I REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 07334/(TELECOMMUNICATION INFORMATION: TELEPHONE: 617-542-8906

TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application GENERAL INFORMATION:
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APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: THE OB RECEPT
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, F
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEC
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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CITY: Boston
STATE: MA
TYPE: amino TOPOLOGY: 1:
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ZIP: 02110-2804
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22-JAN-1996
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TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
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RESULT 24
US-08-638-524A-4
; Sequence 4, Application u.,
; GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: THE OB RECEPTOR AND TITLE OF INVENTION: DIAGNOSIS AND TREAT NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
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                         REFERENCE/DOCKET NUMBER: 0733
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,455
FILING DATE: 22-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/583,153
FILING DATE: 28-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/570,142
FILING DATE: 11-DEC-1995
PRIOR APPLICATION NUMBER: US 08/569,485
FILING DATE: 08-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/566,622
FILING DATE: 04-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/01800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 021001-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/638,524A
FILING DATE: 26-APR-1996
CLASSIFICATION: 536
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                                                                                                                       TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
                                                                                                                                                     SSVKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV
SSVKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV
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US-08-708-123C-4
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acids
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GENERAL INFORMATION:
                                                                                                                                  COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION NUMBER: US/08/708,123C
FILING DATE: 03-SEP-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/583,153
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/583,153
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/569,622
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/562,663
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APPLICATION NUMBER: 08/562,663
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FILING DATE: 08-DEC-1995

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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
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STREET: 27
CITY: Bost
STATE: MA
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ESSEE: Fish & Richardson, |
ET: 225 Franklin Street
: Boston
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Culpepper, Janice A.
White, David W.
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                                                   SSVKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV
                                                                                                                                                                                                                                                                    GSSYEVQVRGKRLDGPGIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCIYKKENKI
                                                                                                                                                                                       VPSKEIVWWMNLAEKIPQSQYDVVSDHVSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH
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COURREST COURTY.

ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows95
SOFTWARE: FastSEQ for Windows Vers
CURRENT APPLICATION NUMBER: US/08/864,5641
FILING DATE: 28-MAY-1997
PRIOR APPLICATION NUMBER: 08/708,123
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/583,524
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/583,153
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/583,153
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
APPLICATION NUMBER: 08/569,485
APPLICATION NUMBER: 08/569,485
APPLICATION NUMBER: 08/569,485
APPLICATION NUMBER: 08/565,622
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 104-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 07-DEC-1995
APPLICATION NUMBER: 08/563,622
FILING DATE: 07-DEC-1995
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US-08-864-564A-4
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APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
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                                                            QQIDANWNIQCWLKGDLKLFICYVESLFKNLFRNYNYKVHLLYVLPEVLEDSPLVPQKGS
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TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
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GENERAL
                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Versio
CURRENT APPLICATION NUMBER: US/10/079,625
FILING DATE: 2002-FEB-19
PRIOR APPLICATION NUMBER: 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/560,485
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/560,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
APPLICATION NUMBER: 35,283
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/01900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: THE OB RECEPT TITLE OF INVENTION: THE DIAGNOSIS TITLE OF INVENTION: INCLUDING OBE NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P STREET: 225 Franklin Street
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TITLE OF INV.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
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CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
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White, David W.
WENTION: THE OB RECEPTOR AND METHODS FOR
VENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
VENTION: INCLUDING OBESITY AND CACHEXIA
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; INFORMATION FOR SEQ
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SEQUENCE CHARACTERISTIC
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GLYVIVPVIISSSILLLGTLLISHQRMKKLFWEDVPNPKNCSWAQGLNFQKPETFEHLFI
                               GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA
                                                              GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED
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Sequence 284, Application US/09948933;
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND CIPID DISORDERS, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL000787
CURRENT APPLICATION NUMBER: US/09/948,933
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/231,399
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 6404
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 284
LENGTH: 1167
TYPE: DDT
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                                                                  LGLHMEITDDGNLKISWSSPPLVPFPLQYQV
                                                                              LGLHMEITDDGNLKISWSSPPLVPFPLQYQVKYSENSTTVIREADKIVSATSLLVDSILP
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iilarity '99.8%;
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                                  DVIYFPPKILTSVGSNVSFHCIYKKENKI 360
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TEFNLNETKPRGKFTYDAVYCCNEHECHH
                       DVIYFPPKILTSVGSNVSFHCIYKKENKI
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Gaps

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RESULT 29
US-09-948-947-87
; Sequence 87, Application US/09948947
; GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENTITLE OF INVENTION: WITH TYPE II DIABETES AND TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000786
; CURRENT APPLICATION NUMBER: US/09/948,947
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,397
; PRIOR APPLICATION NUMBER: 60/231,397
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2172
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 1167
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ORGANISM:
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nes 1163; Conservative
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                                       TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWS:
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                                                                                                       GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSI
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         KHTASVTCGPLLLEPETISEDISVDTSWKNKD:
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99.8%;
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Pred. No.
0; Mismat
        EMMPTTVVSLLSTTDLEKGSVCISDQFN 960
                                                                                                       CVIVSWILSPSDYKLMYFIIEWKNLNED 780
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                                       EDVPNPKNCSWAQGLNFQKPETFEHLFI 900
                                                                       PIFMEGVGKPKIINSFTQDDIEKHQSDA 840
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RESULT 30
US-08-570-142B-4
; Sequence 4, Application US/08570142B
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
            Query Match 82.6%;
Best Local Similarity 99.8%;
Matches 1162; Conservative
                                                                                                                                                                                  APPLICATION NUMBER: US/08/570,142B
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/014001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-8906
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS
TITLE OF INVENTION: FOR THE DIAGNOSIS AND TREAT?
TITLE OF INVENTION: INCLUDING OBESITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson,
STREET: 225 Franklin Street
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Culpepper, Janice A.
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                        Score 962;
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GVTSIKKRESGVLLTDKSRVSCPFPAPCLFT
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                          KDSFSNSSWEIEAQAFFILSDQHPNIISPHL
                         TFSEGLDELLKLEGNFPEENNDKKSIYYL
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 DIRVLQDSCSHFVENNINLGTSSKKTFAS
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; FRAGMENT TYPE:
US-08-570-142C-4
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US-08-570-142C-4
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GENERAL INFORMATION:
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Best Local Similarity
Matches 1162; Conserv
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,142C
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/569,485
                                                                                                                                                                                                                                                                                                   FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-8906
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                             TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS
TITLE OF INVENTION: FOR THE DIAGNOSIS AND TREATH
TITLE OF INVENTION: INCLUDING OBESITY
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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TELEFAX: bi.
200154
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OPERATING SYSTEM:
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COUNTRY: US
ZIP: 02110-2804
                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                                                                                        LENGTH: 1165 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                       GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFAS
QQIDANWNIQCWLKGDLKLFICYVESLFKNLFRNYNYKVHLLYVLPEVLEDSPLVPQKGS
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                                      NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF
                         NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF
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                                                                                                                             Conservative
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internal
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Pred. No. 0;
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PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDLPPTCVLPDSVVKPLSP 540
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                                                  YMPQFQTCSTQTHKIMENKMCDLT
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US-08-582-825-1
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; Sequence 1, Application US/08582825
; GENERAL INFORMATION:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Pessin, Karol M.
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CITY: Thousand Oaks
STATE: California
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CORRESPONDENCE ADDRESS:
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TYPE: amino acid
STRANDEDNESS: single
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STREET: 1840 Dehavilland
                                                                                                                                                                                                                                                                                                                                                                                                                                   RYAELYVIDVNINISCETDGYLTKMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIH
                                                                                                                                                           GSSYEVQVRGKRLDGPGIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCIYKKENKI
PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP
                                                                                  VPSKEIVWWMNLAEKIPQSQYDVVSDHVSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH
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/ENTION: OB PROTEIN RECEPTOR AND RELATED
/ENTION: COMPOSITIONS AND METHODS
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04-JAN-1996
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Pred. No. 0;
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; TOPOLOGY: 1; MOLECULE TYPE: US-08-582-825A-1
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ZIP: 91320-1789
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/582,825A
FILING DATE: 04-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karonim.
                                                                                                                                                                                                         NAME: Pessin, Karol M.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 896 amino acids
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TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED
TITLE OF INVENTION: COMPOSITIONS AND METHODS
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CORRESPONDENCE ADDRESS:
                                                                           Local
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STATE: California
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MICQKECVVLLHWEFIYVITAFNLSYPITPWRFKLSCMPPNSTYDYFLLPAGLSKNTSNS 60
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891; Conserv
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Llarity 100.0%;
Conservative
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                                                                         Score 891; D
Pred. No. 0;
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RESULT 34
US-08-585-005-3
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APPLICANT: Matthews, William
APPLICANT: Bennett, Brian
TITLE OF INVENTION: WSX RECEPTO
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno B
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
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APPLICATION NUMBER: US/08/585,000:
FILING DATE: 08-Jan-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 896 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-585-005-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
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PISEPKDCYLQSDGFYECIFQPIFLLSGYTMW
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nilarity 100.0%;
Conservative 0
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REFERENCE/DOCKET NUMBER: P-40,378
REFERENCE/DOCKET NUMBER: P0986P1
ELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 896 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-667-197-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 35
US-08-667-197-3
                                                                                                                                                                   Query Match 76.5%; S
Best Local Similarity. 100.0%;
Matches 891; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb flop

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/667,197

FILING DATE: 20-Jun-1996
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/5 FILING DATE: 01/08/96 ATTORNEY/AGENT INFORMATION: NAME: Lee, Wendy M. REGISTRATION NUMBER: P-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: USES NUMBER OF SEQUENCES: 47
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STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
COUNTRY: USA
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            QQIDANWNIQCWLKGDLKLFICYVESLFKNLFRNYNYKVHLLYVLPEVLEDSPLVPQKGS
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0; Mismatches
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GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Chiang, Nancy Y.
                                                                                                                                             APPLICANT: Kyung, Jin Kim
APPLICANT: Matthews, William
APPLICANT: Rodrigues, Maria L.
TITLE OF INVENTION: WSX RECEPTOR AC
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                      COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                                                  ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno B
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
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PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP
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FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFOSPLMSVQPINMVKPDPP
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Chiang, Nancy Y.
Kyung, Jin Kim
Matthews, William
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REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P098
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEFAX: 415/952-9881
TELEY: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 806 2012 2013
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Best Local S
Matches 891
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TYPE: Ami
TOPOLOGY:
S-08-779-457-3
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APPLICATION NUMBER: 08/667197
FILING DATE: 06/20/96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/96
ATTORNEY/AGENT INFORMATION:
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RYAELYVIDVNINISCETDGYLTKMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIH
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RESULT 37
US-08-780-562-3
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FILING DATE: 01/08/97
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P098
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEFAX: 415/952-9881
TELEFAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application GENERAL INFORMATION:
                                                                Query Match
Best Local Similarity
Matches 891; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb flog
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US, FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08, FILING DATE: 01/08/97
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bennett, Brian
TITLE OF INVENTION: WSX RECEPTOR
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              SEQUENCE CHARACTERISTICS: LENGTH: 896 amino acid
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Amino Acid
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ER: P0986R1
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                                                              Score 891; DB 11; Length 896; Pred. No. 0; Indels (
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RESULT 38
US-08-585-005-4
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno B
CITY: South San Francisco
STATE: California
COUNTRY: USA
COUNTRY: USA
IP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 M
                                                                                                   APPLICANT: Matthews, William APPLICANT: Bennett, Brian TITLE OF INVENTION: WSX RECEPTOR NUMBER OF SEQUENCES: 45
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,005
FILING DATE: 08-Jan-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEFAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 923 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-585-005-4
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                                       PISEPKDCYLQSDGFYECIFQPIFLLSGYTMW PISEPKDCYLQSDGFYECIFQPIFLLSGYTMW
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TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWS
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                                                                                              RYGLSGKEVQWKMYEVYDAKSKSVSLPV 600
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RESULT 39
US-08-667-197-4
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                                                                                                                                                                          Matches
                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/667,197
FILING DATE: 20-Jun-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                               TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: '
SEQUENCE CHARACTERISTICS:
LENGTH: 923 amino acids
                                                                                                                                                                                                                                                                                                                               NAME: Lee, Wendy M.
REGISTRATION NUMBER: P-40,378
REFERENCE/DOCKET NUMBER: P098
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                     Local Similarity
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GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED
                                                                                                                   GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA
            QQIDANWNIQCWLKGDLKLFICYVESLFKNLFRNYNYKVHLLYVLPEVLEDSPLVPQKGS
                                                               TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
                                                                                                                                                                           891;
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                                                                                                                                                                                                                                                                   Amino Acid
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llarity 100.0%;
Conservative (
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US-08-779-457-4
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                                                                                                                                                      APPLICANT: Chiang, Nancy Y.
APPLICANT: Kyung, Jin Kim
APPLICANT: Matthews, William
APPLICANT: Rodrigues, Maria L.
TITLE OF INVENTION: WSX RECEPTOR AC
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
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                                                                                                 ADDRESSEE: Genentech, Inc
STREET: 460 Point San Brun
CITY: South San Francisco
STATE: California
                                                                                ZIP:
                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                               GLYVIVPVIISSSILLLGTLLISHQRMKKLFWEDVPNPKNCSWAQGLNFQK 891
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GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYP
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FQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMVKPDPP
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GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED
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Carter, Paul J.
Nancy Y.
                                                                                                                                Inc.
Bruno
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FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667197
FILING DATE: 06/20/96
PRIOR APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/96
APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 923 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-779-457-4
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 891; Conservative 0; Mismatches
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VPSKEIVWWMNLAEKIPQSQYDVVSDHVSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH
                                                                                                                                                                                                GSSYEVQVRGKRLDGPGIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVSFHCIYKKENKI
                                      SSVKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV
                                                                            NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF
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RESULT 41
US-08-780-562-4
; Sequence 4, Application US/08780562
; GENERAL INFORMATION:
; APPLICANT: Matthews, William
; APPLICANT: Bennett, Brian
; APPLICANT: WSX RECEPTO
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                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/97
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/
FILING DATE: 01/08/97
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 923 amino acids
                                                                                                   Query Match 76.5%;
Best Local Similarity 100.0%;
Matches 891; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: WSX RECEPTOR NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb fl.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,562
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        841
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STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
               61
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                                          MICQKFCVVLLHWEFIYVITAFNLSYPITPWF
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GASVANFNLTFSWPMSKVNIVQSLSAYPLNS:
             NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFF
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Amino Acid
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                                                                                                                    Score 89
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                                            REKLSCMPPNSTYDYFLLPAGLSKNTSNS 60
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                                                                                                                                  Length 923;
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                                                                                                       Gaps
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Sequence 1, Application US/087/4414;
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
APPLICANT: WELCHER, ANDREW A.
APPLICANT: FLETCHER, FREDERICK A.
TITLE OF INVENTION: OB PROTEIN RECE
TITLE OF INVENTION: COMPOSITIONS AN
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
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US-08-774-414-1
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                           ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavill
CITY: Thousand Oaks
STATE: California
          COUNTRY: UZIP: 91320
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ATTORNEY/AGENT INFORMATION: NAME: Pessin, Karol M. REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version:#1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/671,049
FILING DATE: 27-Sep-2000
PRIOR APPLICATION NUMBER: US/08/774,414
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol M.
REFERENCE/DOCKET NUMBER: A-382-A
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 965 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
TYPE: protein

TYPE: protein
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US-09-671-049-
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GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
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Best Local Similarity
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CITY: Thousand Oaks
STATE: California
COUNTRY: USA
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                                GASVANFNLTFSWPMSKVNIVQSLSAYPLNS: GASVANFNLTFSWPMSKVNIVQSLSAYPLNS:
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RESULT 44
US-08-582-825-5
; Sequence 5, Application US/08582825
; GENERAL INFORMATION:
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED
TITLE OF INVENTION: COMPOSITIONS AND; METHODS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: U.S.A.
21P: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/582,825
FILING DATE: 04-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol M.

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TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
OS-08-582-825-5
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Matches
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                    GEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA
                                                GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED
                                                                           SSVKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAKSKSVSLPV
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RESULT 45
US-08-582-825A-5
US-08-582-825A-5
US-08-5, Application
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-582-825A-5
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, V

CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/582,825A FILING DATE: 04-JAN-1996 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
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CITY: Thousand Oaks
STATE: California
COUNTRY: U.S.A.
ZIP: 91320-1789
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1840 Dehavilland
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RESULT 46
US-08-774-414-5
; Sequence 5, Application US/08774414
; GENERAL INFORMATION:
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                                                                                                                   ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774,414
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol M.
REFERENCE/DOCKET NUMBER: A-382-A
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 969 amino acids
      Query
Best I
                                                        TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: prote
18-774-414-5
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CHANG, MING-SHI
APPLICANT: WELCHER, ANDREW A.
APPLICANT: FLETCHER, FREDERICK A.
TITLE OF INVENTION: OB PROTEIN RECEPTOR
TITLE OF INVENTION: COMPOSITIONS AND MET
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
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RESULT 47
US-08-774-414-6
; Sequence 6, Application U;
; GENERAL INFORMATION:
; APPLICANT: CHANG, MIN
; APPLICANT: WELCHER, A
; APPLICANT: FLETCHER, TITLE OF INVENTION: O
; TITLE OF INVENTION: C
; NUMBER OF SEQUENCES:
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                                                                                                             GASVANFNLTFSWPMSKVNIVQSLSAYPLNS
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                                                                                                                                                                                              SSVKAEITINIGLLKISWEKPVFPENNLQFQ
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PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP
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CHANG, MING-SHI
WELCHER, ANDREW A.
FLETCHER, FREDERICK A.
NVENTION: OB PROTEIN RECEPT
NVENTION: COMPOSITIONS AND
SEQUENCES: 33

AND

METHODS

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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol M.
REFERENCE / COTTORNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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ADDRESSEE: !
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CITY: Th
STATE: C
COUNTRY:
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Local Similarity 100.0%;
les 891; Conservative
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RYAELYVIDVNINISCETDGYLTKMTCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIH
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                                                        PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP
                                                                                                                                     VPSKEIVWWMNLAEKIPQSQYDVVSDHVSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH
                                             PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP
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US-09-671-049-5
; Sequence 5, Application US/09671049
; GENERAL INFORMATION:
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ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/671,04
FILING DATE: 27-Sep-2000
PRIOR APPLICATION NUMBER: US/08/774,4
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol M.
REFERENCE/DOCKET NUMBER: A-387
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 969 amino acids
TYPE: amino acids
TYPE: amino acids
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Matches
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nes 891; Conser
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CORRESPONDENCE ADDRESS:
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ULE TYPE: protein
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                                                                                    76.5%; Score 891; DB 20; Length 969; larity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0; Indels
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COMPOSITIONS AN
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RESULT 49
US-09-671-049-6
; Sequence 6, Application US/09671049
; GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
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NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland D
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
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                                                                                                                              TITLE
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VPSKEIVWWMNLAEKIPQSQYDVVSDHVSKVTFFNLNETKPRGKFTYDAVYCCNEHECHH
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WELCHER, ANDREW A
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                                                                                                             , FREDERICK A.
OB PROTEIN RECEPTOR
COMPOSITIONS AND MES
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COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.
CURRENT APPLICATION NUMBER: US/09/671,
FILING DATE: 27-Sep-2000
PRIOR APPLICATION NUMBER: US/08/774,
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol M.
REFERENCE/DOCKET NUMBER: A-382
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 969 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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Best Local Similarity
Matches 891; Conserv
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REFERENCE/DOCKET NUMBER: A-
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 995 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local Similarity
Matches 891; Conserv
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ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/01 FILING DATE: 04-JAN-1996 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Pessin, Karol M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED
TITLE OF INVENTION: COMPOSITIONS AND METHODS
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CORRESPONDENCE ADDRESS:
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US-09-991-548-6
APPLICANT: NARANDA, Tatjana
TITLE OF INVENTION: RECEPTOR DERIVED PEPTII
TITLE OF INVENTION: OF RECEPTOR ACTIVITY
FILE REFERENCE: 213542000101
CURRENT APPLICATION NUMBER: US/09/991,548
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 09/028,937
PRIOR FILING DATE: 1998-02-24
PRIOR APPLICATION NUMBER: 08/788,820
PRIOR APPLICATION NUMBER: 08/788,820
PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: 08/701,382
PRIOR APPLICATION NUMBER: 08/701,382
PRIOR FILING DATE: 1996-08-22
PRIOR FILING DATE: 1996-08-22
PRIOR APPLICATION NUMBER: 08/612,999
PRIOR FILING DATE: 1996-03-08
                                                                                                                                       Sequence 6, Application US/09991548
GENERAL INFORMATION:
APPLICANT: OLSSON, Lennart
APPLICANT: NARANDA, Tatjana
TITLE OF INVENTION: RECEPTOR DERIV
                                                                                                                                                                                                                                                                                     US-09-994-4
US-09-994-4
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US-10-002-0
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US-09-540-2
US-10-002-0
US-10-003-1
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US-09-520-3
US-09-620-3
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LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human leptin receptor
US-09-991-548-6
                                                                              ; TYPE: PRT; ORGANISM: Homo sapiens US-09-853-180-3
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; SEQ ID NO 8563
; LENGTH: 102
; TYPE: PRT
; ORGANISM: B.fragilis
US-09-540-209B-8563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
US-09-540-209B-8563
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  Query Match
Best Local S
Matches 8
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Best Local
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Best Local Similarity
Matches 23; Conserv
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
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Matches
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                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                     APPLICANT: APPLICANT:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709,1001-001
                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/853,180
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,426
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                      TITLE OF INVENTION: Mammalian Receptor Proteins; FILE REFERENCE: DX01074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/540,209B CURRENT FILING DATE: 2000-04-04
                                                                                                                                                                                                                                                                                                                   APPLICANT: Chirica, Madaline APPLICANT: Parham, Christi 1
                                                                                                                                                                                                                                                                                                                                                   equence 3, Application US/09853180 ENERAL INFORMATION:
                                                                                                                           LENGTH: 1887
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   Similarity
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Similarity 100.0%;
8; Conservative
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0.7%;
larity 100.0%;
Conservative
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ilarity 100.0%;
Conservative
  Score 8; DB 5; Pred. No. 42; 0; Mismatches
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Pred. No.
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                                 Length 1887;
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RESULT 5
PCT-US02-09188-770
; Sequence 770, Application PC/TUS0209188
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
• TITLE OF INVENTION: Human Secreted Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; SEQUENCE US-10-027-400-13
                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                     Matches
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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COMPUTER READABLE FORM:

COMPUTER FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DO

SOFTWARE: Patentin Release #1.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/027,

FILING DATE: 19-Dec-2001

CLASSIFICATION NUMBER: US/08/461,

FILING DATE: 05-JUN-1995

APPLICATION NUMBER: US 07/151,

FILING DATE: 02-FEB-1988

ATTORNEY/AGENT INFORMATION:

NAME: DOW, Karen B.

REGISTRATION UMBER: 29,684

REFERENCE/DOCKET NUMBER: 2307F

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/326-2400
                                                                                                                                                                                                                   Local
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ADDRESSEE: Townsend
STREET: One Market,
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NUMBER OF SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYWSNWSN
                                                                                                                                           MDIKVPM 8
                                                                                                                                                                                                    Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
                                                                                                                                                                                                                                                                                             Contains a phosphate NCE DESCRIPTION: SEQ
                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCES:
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ESCOBEDO, Jaime A.
IVENTION: PLATELET-DER
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                                                                                                                                                                                                                                                                                                                                                       Peptide
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Mismatches
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#1.0, Version #1.30
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Street Tower, 20th Floor
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RESULT 7
PCT-US02-09370-800
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PCT-US02-09188-770
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CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/278,650
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: US 09/950,082
PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US 09/950,083
PRIOR APPLICATION NUMBER: US 09/950,083
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 994
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 507
LENGTH: 50
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CURRENT APPLICATION NUMBER: PCT/US02/09188
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/278,650
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: US 09/950,082
PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US 09/950,083
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 1732
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens PCT-US02-09257-507
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 7
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS957PCT
                                                                                                                                   Sequence 800, Application PC/TUS02
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 770
LENGTH: 50
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Best Local Similarity
TITLE OF INVENTION: Human Secreted Proteins FILE REFERENCE: PS954PCT CURRENT APPLICATION NUMBER: PCT/US02/09370 CURRENT FILING DATE: 2002-03-26 PRIOR APPLICATION NUMBER: US 60/278,650 PRIOR FILING DATE: 2001-03-27 PRIOR APPLICATION NUMBER: US 09/950,082
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                                                                                                                                                                                 Application PC/TUS0209370
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Sequence 3604, Application US/10105299
GENERAL INFORMATION:
APPLICANT: Rosen, et. al
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS950
CURRENT APPLICATION NUMBER: US/10/105,299
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 15197

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US-10-103-295-169
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RESULT 9
US-10-105-299-3604
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; SOFTWARE: PatentIn Ver. 2
; SEQ ID NO 800
; LENGTH: 50
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                               Query Match
Best Local Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US01/29871
PRIOR FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: PCT/US01/00911
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/234,925
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: 09/482,273
PRIOR FILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: PCT/US99/15849
PRIOR APPLICATION NUMBER: PCT/US99/15849
PRIOR FILING DATE: 1998-07-14
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,922
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SEQ ID NO 169
LENGTH: 50
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Best Local
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CURRENT APPLICATION NUMBER: US/10/103,295
CURRENT FILING DATE: 2002-03-22
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TITLE OF INVENTION: 71 Human Secreted
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APPLICATION NUMBER: 60/
                                                              SLDSPPT
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Sequence 6882, Application US/09540209B
GENERAL INFORMATION:
APPLICANT: Gary L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES REL
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 6882
LENGTH: 64
TYPE: PRT
                                                                                                                                                                                                       RESULT 11
US-09-540-2098-6912
; Sequence 6912, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1001-001
; CURRENT APPLICATION NUMBER: US/09/540,209B
; CURRENT FILING DATE: 2000-04-04
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; ORGANISM: B.fragilis
US-09-540-2098-6912
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US-09-540-209B-6882
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US-09-540-209B-6882
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US-10-105-299-3604
RESULT
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Best Local
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SEQ ID NO 6912
LENGTH: 66
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Best Local
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Best Local
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                                                     282 READKIV 288
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RESULT 13
PCT-US02-09921-616
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; LOCATION: (20)
; OTHER INFORMATION:
US-10-103-295-265
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CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: PCT/US01/29871
PRIOR FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: PCT/US01/29871
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/234,925
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: 09/482,273
PRIOR APPLICATION NUMBER: PCT/US99/15849
PRIOR APPLICATION NUMBER: PCT/US99/15849
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR APPLICATION NUMBER: 60/092,922
PRIOR APPLICATION NUMBER: 60/092,925
PRIOR APPLICATION NUMBER: 60/092,926
PRIOR APPLICATION NUMBER: 60/092,956
PRIOR FILING DATE: 1998-07-15
PRIOR FILING DATE: 1998-07-15
PRIOR FILING DATE: 1998-07-15
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 265
LENCTU
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TITLE OF INVENTION: 71 Human Secreted
FILE REFERENCE: PZ030P2
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                                                                                                                     AMSHEY, Stefan R.
DAUGHERTY, Sean C.
DAM, Tam C.
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DAFFO, Abel
JONES, Anissa L.
                                                                                                                                                                        YU, Jimmy Y.
TUASON, Olivia
YAP, Pierre E.
       DAVID, Marie H
LEWIS, Samanth
                                            KLEEFELD, Yael
GERSTIN JR., Edward
PERALTA, Careyna H
                                                                                                                                                                                                                                                                                   TRAN, Alanna-Phung B
DAHL, Christopher R.
                                                                          LIU, Tommy F.
NGUYEN, Duy-Viet An
KLEEFELD, Yael
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CHINN, Joyce
                                                                                                                                                                                                                      DUFOUR, Gerard E
HILLMAN, Jennifer
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RESULT 14
US-09-620-393B-6470
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Best Local
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                                                                                                                           NAME/KEY: misc_feature
LOCATION: 1..122
OTHER INFORMATION: Ceres
-09-620-393B-6470
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PRIOR FILING DATE: 2001-03-29; 2001-03-29; 2001-05-16; 2001-05-17; 2001-05-17; 2001-06-19; 2001-06-20; 2001-06-20
NUMBER OF SEQ ID NOS: 1146
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/620,393B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9948
                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1068P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SECRETORY MOLECULES FILE REFERENCE: PT-1232 PCT
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OTHER INFORMATION:
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ORGANISM: Homo sapiens
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LENGTH: 86
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ORGANISM: Arabidopsis thaliana
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LENGTH: 122
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Bernard
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RESULT

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US-10-106-698-6272; Sequence 6272; A
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US-10-106-698-7726
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APPLICANT: Ruben et al.
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
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Best Local
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                                                                           OTHER INFORMATION: Xaa E NAME/KEY: MISC_FEATURE LOCATION: (39)
OTHER INFORMATION: Xaa E NAME/KEY: MISC_FEATURE
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OTHER INFORMATION: Xaa e NAME/KEY: MISC_FEATURE LOCATION: (20)
OTHER INFORMATION: Xaa e
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
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CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
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                                LOCATION: (56)
OTHER INFORMATION:
NAME/KEY: MISC_FEA
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 OTHER INFORMATION: Xaa
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2000-09-28
NUMBER: US 60/157,137
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Sequence 282, Application PC/TUS0207826

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc. et al.

TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For

TITLE OF INVENTION: Assessment, Prevention, and Therapy of

FILE REFERENCE: MRI-030PC

CURRENT APPLICATION NUMBER: PCT/US02/07826

CURRENT FILING DATE: 2002-03-14

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/276,026

PRIOR APPLICATION NUMBER: 60/324,967

PRIOR APPLICATION NUMBER: 60/324,967

PRIOR APPLICATION NUMBER: 60/325,102

PRIOR APPLICATION NUMBER: 60/325,102

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-19

PRIOR FILING DATE: 2001-09-19
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PCT-US02-07826-282
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Best Local Similarity
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GENERAL I
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SEQ ID NO 282
                                                                           APPLICANT:
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                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                       John MONAHAN
Manjula GANNAVARAPU
                                                                                                                       Sebastian HOERSCH
Shubhangi KAMATKAR
Steve G. KOVATS
Rachel E. MEYERS
Michael MORRISEY
Peter OLANDT
                                                         Gordon Robert
Xumei ZHAO
Karen GLATT
             Rosemarie SCHMANDT
Xumei ZHAO
                                              Karen LU
                                                                                           Peter VEIBY
                                                                                                         Ami SEN
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C. BAST, Jr
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CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT FILING DATE: 2002-04-19
Prior Application removed - See File Wrapper
NUMBER OF SEQ ID NOS: 646
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 456
LENGTH: 197
TYPE: PRT
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PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-09/26
PRIOR PILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 282
LENGTH: 176
В
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; NAME/KEY: misc_feature
; LOCATION: (183)
; OTHER INFORMATION: Xaa equals
US-10-125-540-456
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-340-282
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                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids,
FILE REFERENCE: PTZ14C1
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174 LLPAGLS 180
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RESULT 20 US-10-106-698-6320 ; Sequence 6320, App. ; GENERAL INFORMATION

e 6320, Application US/10106698 INFORMATION:

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RESULT 22
US-09-540-209B-8108
; Sequence 8108, Application US/09540209B
; GENERAL INFORMATION:
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; ORGANISM: Hordeum Vulgare
PCT-US01-46651-2
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SEQ ID NO 2
LENGTH: 229
APPLICANT: Gary L. Breton TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.1001-001 CURRENT APPLICATION NUMBER: US/09/540,209B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: PCT/US01/46651
CURRENT FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 60/247,161
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CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Von Wettstein, Diter TITLE OF INVENTION: Plant Promoters, and Methods FILE REFERENCE: WSUR118192
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TITLE OF INVENTION: Colon and Colon Cancer
FILE REFERENCE: PA005P1
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ID NOS: 8564
entIn Ver. 3.0
                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                               Score 7; DB 1; Pred. No. 60; 0; Mismatches
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                                                                                                                                                                                                                                                                                                 Length 229;
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                                                   TO BACTEROIDES
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; ORGANISM: B.fragilis
US-09-540-209B-8108
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US-10-138-632-2
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SEQ ID NO 8108
LENGTH: 259
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Best Local Similarity 100.
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                                                       INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                              49 LPAGLSK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 LPAGLSK 31
                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
MOLECULE TYPE: |
ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                     PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                FILING DATE: 06-May-2002 CLASSIFICATION: <Unknown>
                                  TYPE: amino acid
                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                       STATE: VIRGINIA COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: ARLINGTON
                                                                                                         TELEPHONE:
                                                                                                                                                                                                                  APPLICATION NUMBER: 09/455,406
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/708,856
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ozaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ochiai, Keiko
Chiba, Shigeru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ando,
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                                                                                  248545
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                                                                                              703-312-6666
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Cis-3-Hydroxy
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-L-Proline
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GENERAL INFORMATION: GENERAL INFORMATION: 94 Human Secreted Proteins TITLE OF INVENTION: 94 Human Secreted Proteins FILE REFERENCE: PZ029G30AP1D2
CURRENT APPLICATION NUMBER: US/10/115,123
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: PCT/US99/13418
PRIOR FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 60/089,507
PRIOR FILING DATE: 1998-06-16
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US-10-115-123-331
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; LOCATION: (134)
; OTHER INFORMATION:
US-10-115-123-233
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Best Local Similarity
Thickes 7; Conserve
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CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: PCT/US99/13418
PRIOR FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 60/089,507
PRIOR APPLICATION NUMBER: 60/089,508
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,509
PRIOR APPLICATION NUMBER: 60/089,509
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,510
PRIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 1998-06-16
                                                                                                                                                                             Sequence 331, Application US/10115123 GENERAL INFORMATION:
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LENGTH: 293
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TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: PZ029G30AP1D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 199 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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les 7; Conser
APPLICATION NUMBER: 60/089,508 FILING DATE: 1998-06-16
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FILING DATE: 1998-06-22
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PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,510
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/090,112
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090,113
PRIOR FILING DATE: 1998-06-22
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Matches
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Best Local
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LENGTH: 307
                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/125,54(
CURRENT FILING DATE: 2002-04-19;
Prior Application removed - See File Wraphumber of SEQ ID NOS: 646;
SOFTWARE: Patentin Ver. 2.0;
SEQ ID NO 294;
LENGTH: 358;
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens US-10-125-540-294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: SITE
; LOCATION: (148)
; OTHER INFORMATION:
US-10-115-123-331
                                                                                                                                            Sequence 225, Application US/09994404 GENERAL INFORMATION:
APPLICANT: ESSER, KLAUS M.
APPLICANT: CHAN, JOHN Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 294, Application US/10125540 GENERAL INFORMATION:
APPLICANT: SUTTON, DAVID
TITLE OF INVENTION: NOVEL CODING SEQUENCES FROM HERPES
TITLE OF INVENTION: SIMPLEX VIRUS TYPE-2
FILE REFERENCE: P50583
CURRENT APPLICATION NUMBER: US/09/994,404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids,
FILE REFERENCE: PTZ14C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 532 SOFTWARE: Patentin Ver. 2
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7; Conser
                                                                         DABROWSKI-AMARAL,
DELVECCHIO, ALFREI
DILLON, SUSAN B.
LEARY, JEFFREY JOS
                                                                                                                                                                                                                                                                                                                                              Conservative
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Conservative
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D MICHAEL
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No. 78;
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; TYPE: PRT
; ORGANISM: Herpes simplex
US-09-994-404-225
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US-09-994-404-28
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                                                                                  RESULT 29
US-09-994-404-158
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CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 09/297,477
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: US 60/049,018
PRIOR APPLICATION NUMBER: US 60/049,018
PRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 7; Conserv
        Sequence 158, Application US/09994404
GENERAL INFORMATION:
APPLICANT: ESSER, KLAUS M.
APPLICANT: CHAN, JOHN Y.
APPLICANT: DABROWSKI-AMARAL, CHRIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28, Applica GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 303
SOFTWARE: FastSEQ for Windows
SEQ ID NO 225
LENGTH: 461
                                                                                                                                                                                                                                                                                               SEQ ID NO 28
LENGTH: 470
TYPE: PRT
ORGANISM: Herpes simplex
                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                           Query Match
Best Local
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PRIOR APPLICATION NUMBER: US 60/030,279
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: US 60/049,018
PRIOR FILING DATE: 1997-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SUTTON, DAVID
TITLE OF INVENTION: NOVEL CODING SEQUENCES
TITLE OF INVENTION: SIMPLEX VIRUS TYPE-2
FILE REFERENCE: P50583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ESSER, KLAUS MAPPLICANT: CHAN, JOHN Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR
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                                                                                                                                                                             855
                                                                                                                                                  231 LLLGTLL 237
                                                                                                                                                                                                                          Local
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APPLICATION NUMBER: 09/297,477
                                                                                                                                                                LLLGTLL 861
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                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                              FastSEQ
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LEARY, JEFFREY JOSEPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09994404
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ALFRED
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           CHRISTINE
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0. 1.1e+02;
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o. 1.2e+02;
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PRIOR APPLICATION NUMBER: 09/297,477

PRIOR FILING DATE: 1999-06-29

PRIOR FILING DATE: 1999-06-29

PRIOR FILING DATE: 1999-11-04

PRIOR APPLICATION NUMBER: US 60/030,279

PRIOR APPLICATION NUMBER: US 60/049,018

PRIOR FILING DATE: 1997-06-09

NUMBER OF SEQ ID NOS: 303

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 158

LENGTH: 470

TYPE: DDM
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PCT-US02-09944-442
PCT-US02-09944-442
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APPLICANT: LAN, Ruth Y.

APPLICANT: URASHKA, Michael E.

TITLE OF INVENTION: MOLECULES FOR DISEASE
FILE REFERENCE: PT-1231 PCT
CURRENT APPLICATION NUMBER: PCT/US02/0994/
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: 60/280,067; 60/291,829; 60/299,428; 60/300,001; 60/29PRIOR FILING DATE: 2001-03-29; 2001-03-28
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Best Local
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                                                                                                                                                                   APPLICANT:
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CURRENT FILING DATE: 2001-11-26
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                                                                                                                                                                                              DAVID, Marro
LEWIS, Samantha &
CHEN, Alice J.
                                                                                                                                                                                                                                           NGULL
KLEEFELD, YAGE
GERSTIN, JR., Edward
GERSTIN, Careyna H.
                                                                                                                                                                                                                                                                                                                                                                              YU, Jimmy Y.
TUASON, Olivia
YAP, Pierre E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INCYTE GENOMICS,
                                                                                                                                                                   HARRIS, FLORES,
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LEARY, JEFFREY JOSEPH
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                                                                                                                                                                                                                                                                                                    DAM, Tam C.
LIU, Tommy F.
NGUYEN, Duy-Viet An
                                                                                                                                                                                                                                                                                                                                                    AMSHEY, Stefan R.
DAUGHERTY, Sean C.
                                                                                                                                                                                                                                                                                                                                                                                                                           CHINN, Joyce
DUFOUR, Gerard E.
HILLMAN, Jennifer
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                                                                                                                                                                                            PANZER,
                                                                                                                                    LO, Audrey
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                                                                                          FOR DISEASE DETECTION AND TREATMENT
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Pred. No
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No. 1.2e+02;
atches 0;
0/279,619; 60/280,068; 60/291,280; 60/291,8 0/299,776 28; 2001-03-29; 2001-05-16; 2001-05-17;
                                                             944
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US-10-002-050-8
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; OTHER INFORMATION: Incyte
PCT-US02-09944-442
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NUMBER OF SEQ ID NOS: 792
SOFTWARE: PERL Program
SEQ ID NO 442
LENGTH: 473
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SEQ ID NO 8
LENGTH: 473
TYPE: PRT
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Best Local S
Matches 7
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Best Local Similarity 100.0%;
Matches 7; Conservative
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APPLICANT: Herrmann, John
TITLE OF INVENTION: Novel Nucleic Acid Sequences
FILE REFERENCE: 15966-554 Cura-54 CON-S14
CURRENT APPLICATION NUMBER: US/10/002,050
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 09/604,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Herrmann, John
TITLE OF INVENTION: Polynucleotides and polypeptides
FILE REFERENCE: 15966-554 Cura-54 CON-S8
CURRENT APPLICATION NUMBER: US/10/002,304
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 09/604,286
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/140,584
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 49
                                                                                             APPLICANT:
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                                                                                       Vernet, Corine
Yang, Meijia
Boldog, Ferenc
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Yang, Meijia
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1.2e+02;
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hes 0;
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; ORGANISM: Homo sapiens
US-10-003-152-8
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US-10-115-123-158
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US-10-003-152-8
; Sequence 8, Application US/10003152
; GENERAL INFORMATION:
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APPLICANT: Ruben et al.
TITLE OF INVENTION: 94 Human Secreted Profile REFERENCE: PZ029G30AP1D2
CURRENT APPLICATION NUMBER: US/10/115,123
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: PCT/US99/13418
PRIOR FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 60/089,507
PRIOR APPLICATION NUMBER: 60/089,508
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,508
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Best Local Similarity
7; Conserv
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TITLE OF INVENTION: Novel Amino Acid Sequence of Invention of Inventio
                                                                                                                                                                                                                                                                                                                                                            Sequence 158, Application US/10115123 GENERAL INFORMATION:
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LENGTH: 47
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APPLICANT:
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NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
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PRIOR APPLICATION NUMBER: 60/140,584
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 49
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Yang, Meijia
Boldog, Ferenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Mismatches 0
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Mismatches 0; Indels
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S12
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Best Local
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SEQ ID NO 332
LENGTH: 504
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PRIOR
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EQ ID NO 158
LENGTH: 490
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NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-06-22
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OTHER INFORMATION:
                                                                                                          LOCATION: (148)
OTHER INFORMATION:
                                                                                                                                FEATURE:
NAME/KEY: SITE
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                                                                       OTHER INFORMATION:
                                                                                 NAME/KEY: SITE LOCATION: (403)
                                                                                                                                                            ORGANISM: Homo
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les 7; Conserv
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APPLICATION NUMBER: 60/
FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/090,113
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                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60,
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Query Match
Best Local Similarity

Score Pred.

DB 6; Length 504; 1.2e+02;

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RESULT 37
US-09-540-209B-10008
- Segmence 10008, Application US/09540209B
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; SEQ ID NO 1433
; LENGTH: 578
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-573-655B-1433
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SEQ ID NO 10008
LENGTH: 642
TYPE: PRT
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APPLICANT: SOLOVYEV, Victor and TROUKH
                                                                   Sequence
GENERAL I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
                                                                                                                                                                                      Matches
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APPLICANT: GARY L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND
TITLE OF INVENTION: FOR DIAGNOSTICS
FILE REFERENCE: 2709.1001-001
CURRENT APPLICATION NUMBER: US/09/54C
CURRENT FILING DATE: 2000-04-04
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Best Local
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            APPLICANT:
                         APPLICANT:
                                                       APPLICANT:
 APPLICANT:
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                                                                                                                                                               857
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                                                                                                                                         138 LGTLLIS 144
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                                                                                           01339-2
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                                                                   2, Application PC/TUS0201339 INFORMATION:
                                                                                                                                                     LGTLLIS 863
                                                                                                                                                                                    Similarity 100 7; Conservative
                                                                                                                                                                                                                                                                                                      SEQ ID NOS: 10444
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                                                          INCYTE GENOMICS,
BAUGHN, Mariah R.
AZIMZAI, Yalda
TANG, Y. Tom
                              WALIA, Narinder K.
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red. No. 1.5e+02;
Mismatches 0; Indels
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). 1.4e+02;
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DNA Fragments
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; ORGANISM: Homo sapiens
US-10-002-304-6
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US-10-002-304-6
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NAME/KEY: misc_feature

OTHER INFORMATION: Incyte ID

PCT-US02-01339-2
                             PRIOR FILING DATE: 1999
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver.
SEQ ID NO 6
LENGTH: 788
TYPE: PRT
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Best Local
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                                                                                                                                      APPLICANT: Boldog, Ferenc
APPLICANT: Boldog, Ferenc
APPLICANT: Herrmann, John
TITLE OF INVENTION: Polynucleotides and polypeptides encoded thereby
FILE REFERENCE: 15966-554 Cura-54 CON-58
CURRENT APPLICATION NUMBER: US/10/002,304
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 09/604,286
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/140,584
PRIOR APPLICATION NUMBER: 60/140,584
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TITLE OF INVENTION: RECEPTORS AND MEMBRANE-ASSOCIATED PROTEINS
FILE REFERENCE: PI-0346 PCT
FILE REFERENCE: PI-0346 PCT
CURRENT APPLICATION NUMBER: PCT/US02/01339
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 60/262,838; 60/265,927; 60/271,196; 60/274,549; 60/334,179
PRIOR FILING DATE: 2001-01-19; 2001-02-02; 2001-02-23; 2001-03-09; 2001-11-28
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SOFTWARE: PERL Program
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SWARNAKAR, Anı...
RAMKUMAR, Jayalaxmi
POTYEN, Danniel B.
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Vernet, Corine
Yang, Meijia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAFALIA, April J.A. ELLIOTT, Vicki S. KALLICK, Deborah A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KHAN, Farrah A.
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                                                                                                                                                                                                                                                                                                                                                                                       Richard
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Query Match

0.6%;

Score

DB 6;

Length 788;

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APPLICANT: Herrmann, John
ITITLE OF INVENTION: Novel Amino Acid Sequence of the Reference: 15966-554 Cura-54 CON-S1:
CURRENT APPLICATION NUMBER: US/10/003,15:
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 09/604,286
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/140,584
PRIOR APPLICATION NUMBER: 60/140,584
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 788
TYPE: PRT
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-050-6
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US-10-002-050-6
                                                                    ; ORGANISM: Homo US-10-003-152-6
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Best Local Similarity
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Best Local
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Herrmann, John
TITLE OF INVENTION: Novel Nucleic Acid
FILE REFERENCE: 15966-554 Cura-54 CON-
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Shimkets, Richard
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Yang, Meijia
Boldog, Feren
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Yang, Meijia
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4 CON-S12
10/003,152
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Mismatches 0;
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S14
050
; DB 6; Length 788; No. 1.8e+02;
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RESULT 44
US-10-128-714-3585; Sequence 3585, Appli
; GENERAL INFORMATION:
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US-09-573-655B-2349
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US-09-540-209B-5548
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// ORGANISM: Arabidopsis thaliana
US-09-573-655B-2349
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US-09-540-209B-5548
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Best Local Similarity
7; Conserve
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SEQ ID NO 2349
LENGTH: 951
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GENERAL INFORMATION:
APPLICANT: Gary L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2349, Application US/09573655B GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 10444
EQ ID NO 5548
LENGTH: 885
                            APPLICANT:
                                                                    APPLICANT:
                                                                            APPLICANT: Jiang,
                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/573,655B CURRENT FILING DATE: 2000-05-18
                                          APPLICANT:
                                                      APPLICANT:
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                APPLICANT:
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: Eroshkin, Alexey M
: Lemieux, Sebastien M
INVENTION: Identification
                                                                                                                                                                                                                                                                                                                                                          PatentIn version 3.0
                                     Hu, Wengi
Tishkoff, Daniel
Zamudio, Carlos
                                                                                                        Application
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   of.
 Essential Genes
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Aspergillus
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                         939 VVSLLST 945
                                                             Local
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; ORGANISM: Aspergillus US-10-128-714-8585
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                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
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PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                     SEQ ID NO 8585
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use.
FILE REFERENCE: 10182-018-999
                                                                                                                                                                            NUMBER OF SEQ ID NOS: 8603
SOFTWARE: Paten+T
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                                                                                                                                                  LENGTH: 1018
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                   Similarity
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Tishkoff, Daniel
Zamudio, Carlos
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 Conservative
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                                      Score 7;
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No. 2.3e+02;
natches 0; Indels
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APPLICANT: Oomen, Raymond P.

TITLE OF INVENTION: Identification of Polynucleotides

TITLE OF INVENTION: Encoding Novel Helicobacter Polypep

TITLE OF INVENTION: Genome

FILE REFERENCE: 06132/043002

CURRENT APPLICATION NUMBER: US/09/895,913A

CURRENT FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: US 08/881,227

PRIOR FILING DATE: 1997-06-24

NUMBER OF SEQ ID NOS: 368

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 246
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US-09-895-913A-246
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Best Local
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ORGANISM: Helicobacter pylori
-09-895-913A-246
              APPLICANT: MARQUIS, JOSEPH P.

APPLICANT: MARQUIS, JOSEPH P.

APPLICANT: KABLE, AMY E.

TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT

FILE REFERENCE: PF-0921 PCT

CURRENT APPLICATION NUMBER: PCT/US02/09809

CURRENT FILING DATE: 2002-03-29

PRIOR APPLICATION NUMBER: 60/280,387; 60/282,335; 60/286,663; 60/285,484; 60/350,702;

PRIOR FILING DATE: 2001-03-30; 2001-04-05; 2001-04-13; 2001-04-19; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18; 2002-01-18;
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APPLICANT: Kleanthorn
NUMBER
                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                              THANGAVELU, KAVITHA YAO, MONIQUE G. ELLIOTT, VICKI S. BAUGHN, MARIAH R. EMERLING, BROOKE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kleanthous, Harold
Al-Garawi, Amal
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LU, DYUNG AINA M.
ARVIZU, CHANDRA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRAN, b...
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YUE, HENRY
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                                                                                                                                                                                                                                                                 GIETZEN, KIMBERLY J
BECHA, SHANYA D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARVIZU, CHANDRA S
GANDHI, AMEENA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAMKUMAR, JAYALAXMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miller, Charles
Tomb, Jean Francois
Oomen, Raymond P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WARREN, BRIDGET A. NGUYEN, DANNIEL B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWARNAKER,
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NOS:
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Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5; io. 2.7e+02; 0;
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RESULT 49
US-10-106-698-7746
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US-09-423-037A-17
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; NAME/KEY: misc_feature;
; OTHER INFORMATION: Incy
PCT-US02-09809-5
           CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: HEERY, DAY
APPLICANT: PARYTTITIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: PARKER, MALCOLM GEORGE
TITLE OF INVENTION: INHIBITORS OF NUCLEAR
TITLE OF INVENTION: INTERACTION
FILE REFERENCE: 009901/0264015
CURRENT APPLICATION NUMBER: US/09/423,03;
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/GB98/01238
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: GB 9708676.3
PRIOR FILING DATE: 1997-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER: PA
SOFTWARE: PA
SEQ ID NO 17
SEQ ID NO 17
                                                                                                                                                                                               Sequence 7746, Application US/10106698 GENERAL INFORMATION:
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Best Local
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                                                                                                                                               APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Car
FILE REFERENCE: PA005P1
  NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Unknown Organism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description of Unknown Organism: DNA binding domain SRCla peptide
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                                                                                                                                                                                                                                                                                                                                                                            Score 6;
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No. 9.2e+04;
atches 0; Indel:
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No. 3.4e+02;
atches 0; Indels
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APPLICANT: ROSENTHAL, ANDRE
TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FRO
FILE REFERENCE: ALBRE 11
CURRENT APPLICATION NUMBER: US/09/623,791A
CURRENT FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: PCT/DE99/00721
PRIOR FILING DATE: 1999-03-09
NUMBER OF SEQ ID NOS: 201
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 134
LENGTH: 30
TYPE: PRT
ORGANISM: Homo sapiens
US-09-623-791A-134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (2)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (10)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (16)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (19)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (19)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-7746
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US-09-623-791A-134
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LENGTH: 27
TYPE: PRT
                                                                        Query Match 0.5
Best Local Similarity 100
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 134, Application US/09623791A
GENERAL INFORMATION:
APPLICANT: SPECHT, THOMAS
APPLICANT: HINZMANN, BERND
APPLICANT: SCHMITT, ARMIN
APPLICANT: PILARSKY, CHRISTIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.1
Best Local Similarity 100
Matches 6; Conservative
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576 LSGKEV 581
||||||
23 LSGKEV 28
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                                                                                           0.5%;
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                                                                       Score 6; DB 5; pred. No. 91; 0; Mismatches
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Search completed: May 18, Job time: 258 sec

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RESULT 1
US-08-599-455B-4
; Sequence 4, Application US/08599455B:
; Patent No. 5972621
; GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMFOUNDS THAT
TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
; NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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; TYPE: amino acid
; TOPOLOGY: unknown
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; FRAGMENT TYPE: inter
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Best Local S
Matches 1165
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OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,455B
FILING DATE: 22-JAN-1996
PRIOR APPLICATION NUMBER: U8/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
APPLICATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/017001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-8906
TELEX: 200154
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
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                                                                                                              APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AN
TITLE OF INVENTION: THE DIAGNOSIS AND
TITLE OF INVENTION: INCLUDING OBESITY
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Pint
                                                                                                                                                                                                                                     Sequence 4, Application Patent No. 6287782 GENERAL INFORMATION:
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows V.
CURRENT APPLICATION DATA:
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CITY: Boston
STATE: MA
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           Ver:
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; MOLECULE TYPE:
; FRAGMENT TYPE:
US-09-069-781B-4
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Best Local Similarity
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: US 08/569,485
FILING DATE: 08-DEC-1995
FILING DATE: 08-DEC-1995
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D.,
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 0
FILING DATE: 26-APR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1165 amino acids
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                                      LGLHMEITDDGNLKISWSSPPLVPFPLQYQVKYSENSTTVIREADKIVSATSLLVDSILP
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03-SEP-1996
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28-MAY-1997
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27-NOV-1995
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22-JAN-1996
MBER: US 08/583,153
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                                                                SEQ ID NO 1
LENGTH: 11
TYPE: PRT
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GENERAL INFORMATION:
                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/093,81
CURRENT FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/049,108
PRIOR FILING DATE: 1997-06-09
                                                                                                                                                                                       APPLICANT: Carpenter et al.
TITLE OF INVENTION: ASSAY SYSTEMS
FILE REFERENCE: REG 580-A
                                                                                                       SOFTWARE:
                                                                                                                    NUMBER OF SEQ ID NOS:
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TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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Patent No
                                                                                                                                                                                                                                                                                                                                                                 STREET: 1155 Avenue of The Americas CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,957A
FILING DATE: 20-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
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APPLICATION NUMBER: 008907-0033
REFERENCE/DOCKET NUMBER: 008907-0033
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Ec
STREET: 1155 Avenue of
CITY: New York
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MOLECULE TYPE:
18-618-957A-11
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Local Similarity 99.9%;
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AL INFORMATION:
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                                             GVTSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFAS
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GASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED
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                                                                                                                                            KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMMPTTVVSLLSTTDLEKGSVCISDQFN
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TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI
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STREET: 1155 Avenue of The Amel
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VETSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,
FILING DATE: 20-MAR-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: EPILING DATE:
APPLICATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 0089
TELECOMMUNICATION INFORMATION:
TELEFHONE: 650-493-4935
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 896 amino acids
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-618-957A-10
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Best Local S
Matches 781
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APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas Joel
APPLICANT: Shafer, Alan Wayne
TITLE OF INVENTION: METHODS FOR US:
TITLE OF INVENTION: GENE AND ITS GI
TITLE OF INVENTION: DEVELOPMENT
NUMBER OF SEQUENCES: 28
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CORRESPONDENCE ADDRESS:
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EDSPLVPQKGSFQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFRSPLMSV 229
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TFVSTVNSLVFQQIDANWNIQCWLKGDLKLFICYVESLFKNLFRNYNYKVHLLYVLPEVL 169
QPINMVKPDPPLGLHMEITDDGNLKISWSSPPLVPFPLQYQVKYSENSTTVIREADKIVS 289
QPINMVKPDPPLGLHMEITDDGNLKISWSSPPLVPFPLQYQVKYSENSTTVIREADKIVS 289
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R: 008907-0033-999
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                                                                                                                                         APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A NOTITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the America
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTUMBER: BESTEE: PC-DOS/MS-DOS
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APPLICANT: C
APPLICANT: Z
APPLICANT: S
              REFERENCE/DOCKET NUMBER: 89: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION:
                                            APPLICATION NUMBER: US/08/693,697
FILING DATE: 05-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: POISSANT, Brian M.
REGISTRATION NUMBER: 28,462
                                                                                                                       SOFTWARE: FastSEQ for Windows CURRENT APPLICATION DATA:
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Cioffi, Joseph
Ciorancic, Thomas J.
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650-493-5556
                                    8907-0037-999
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
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Best Local
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hes 781;
                                                         QDDIEKHQSDAGLYVIVPVIISSSILLLGTLLISHQRMKKLFWEDVPNPKNCSWAQGLNF
                                                                                               HTVTVLAINSIGASVANENLTESWPMSKVNIV
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LPDSVVKPLPPSSVKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVY 591
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QPINMVKPDPPLGLHMEITDDGNLKISWSSPPLVPFPLQYQVKYSENSTTVIREADKIVS
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                              QDDIEKHQSDAGLYVIVPVIISSSILLLGTLI
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Similarity 99.9%;
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                                                                                                INHHTSCNGTWSEDVGNHTKFTFLWTEQA
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US-08-618-957A-9
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NAME: POISSANT, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 0089
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEFAX: 650-493-5556
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9,
Patent No.
GENERAL II
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Shafer, Alan Wayne TITLE OF INVENTION: METHODS FOR USING TITLE OF INVENTION: GENE AND ITS GENE TITLE OF INVENTION: DEVELOPMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE
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STREET: 11
CITY: New
STATE: NY
                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                                                                                                                                                                                 Local Similarity
les 781; Conserv
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                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                  ATSILVDSILPGSSYEVQVRGKRLDGPGIWSDWSTPRVFTTQDVIYFPPKILTSVGSNVS
                                                                                        EDSPLVPQKGSFQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSV 229
EDSPLVPQKGSFQMVHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFRSPLMSV 229
FHCIYKKENKIVPSKEIVWWMNLAEKIPQSQYDVVSDHVSKVTFFNLNETKPRGKFTYDA
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larity 99.9%;
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Sequence 33, Applicate Patent No. 5869610 GENERAL INFORMATION:
                                                                       ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: FastSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/693,697

FILING DATE: 05-AUG-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Poissant, Brian M.

REGISTRATION NUMBER: 28,462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A
TITLE OF INVENTION: RECEPTOR
               REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                             STREET: 1155 AV
CITY: New York
STATE: New York
COUNTRY: USA
TELEPHONE:
TELEFAX:
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LPDSVVKPLPPSSVKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVY 589
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SLYCSDIPSIHPISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCV 529
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FIIEWKNLNEDGEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFT 829
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; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3
; SEQUENCE CHARACTERISTICS:
; LENGTH: 908 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
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QPINMVKPDPPLGLHMEITDDGNLKISWSSPPLVPFPLQYQVKYSENSTTVIREADKIVS
                                                                HTVTVLAINSIGASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMY
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; TYPE: amino acid
; STRANDEDNESS: sing
; TOPOLOGY: linear
; MOLECULE TYPE: prote
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US-08-618-957A-8
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618
FILING DATE: 20-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 0089
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEFAX: 650-493-5556
TELEFAX: 65141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 958 amino acids
TYPE: -amino acids
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Best Local Similarity
Matches 781; Conserv
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APPLICANT: Cioffi, Joseph
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas Joel
APPLICANT: Shafer, Alan Wayne
TITLE OF INVENTION: METHODS FOR USING
TITLE OF INVENTION: GENE AND ITS GENE
TITLE OF INVENTION: DEVELOPMENT
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
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STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER BEARLE
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RESULT 10
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APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION NUMBER: US/08/355,888A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: POISSANT, Brian M.
DESTINATION: METALEMENT METALEMETALEMENT METALEMENT METALEMETALEMETALEMENT METALEMENT METALEMETALEMETALEMETALEMETALEMETALEMETALEMETALEMETALEMETALEMETALEMETALEMETALEM
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7225
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
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STREET: 1155 Avenue of the
CITY: New York
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Best Local S
Matches 781
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TOPOLOGY: linear
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mes 781; Conser
                              HTVTVLAINSIGASVANFNLTFSWPMSKVNIVQSLSAYPLNSSCVIVSWILSPSDYKLMY 769
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               QK 891
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                                                                        FIIEWKNLNEDGEIKWLRISSSVKKYYIHDHFIPIEKYQFSLYPTFMEGVGKPKIINSFT 829
                                                                                                                                                                                                LPDSVVKPLPPSSVKAEITINIGLLKISWEKPV
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RESULT 11 US-08-693-697-8

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APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Amer.
CITY: New York
STATE. No. 1000
                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                        NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 890;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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Conservative
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2R: 8907-0037-999
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RESULT 12
US-08-640-389A-3
; Sequence 3, Applica
; Patent No. 5912123
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                                             SOFTWARE: Patentin Release #1.0, Ver CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,389A FILING DATE: 29-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-032
RELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zupancic, Thomas
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: DETECTIC
TITLE OF INVENTION: RECEPTOR
TITLE OF INVENTION: REGULAT:
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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CITY: New York
STATE: New York
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TOPOLOGY: 14
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| QDDIEKHQSDAGLYVIVPVIISSSILLLGTLLISHQRMKKLFWEDVPNPKNCSWAQGLNF 891
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TYPE:

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RESULT 13
US-08-693-696-8
; Sequence 8, Application U
; Patent No. 6005080
; GENERAL INFORMATION:
; APPLICANT: Snodgrass,
APPLICANT: Cioffi, Jc
; APPLICANT: Zupancic,
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illarity 99.9%;
Conservative
Snodgrass, H. R. Cioffi, Joseph Zupancic, Thomas
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; LENGTH: 960 amino a
; TYPE: amino acid
; TOPOLOGY: linear
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REFERENCE/DOCKET NUMBER: 7225-07
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 amino acido
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Best Local Similarity 99.9%;
Matches 781; Conservative
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ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the America.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Shafer, A TITLE OF INVENTION: I TITLE OF INVENTION: NUMBER OF SEQUENCES:
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                      QPINMVKPDPPLGLHMEITDDGNLKISWSSPPL
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EDSPLVPQKGSFQMVHCNCSVHECCECLVPVPT
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LPDSVVKPLPPSSVKAEITINIGLLKISWEKPV
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Hu-B1.219
RECEPTOR
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FPENNLQFQIRYGLSGKEVQWKMYEVY 589
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; MOLECULE TYPE: US-08-588-190-3

protein

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GENERAL INFORMATION:
APPLICANT: Snodgrass, H. Ralph
APPLICANT: Cloff!, Joseph
APPLICANT: Zupancic, Thomas Joel
APPLICANT: Shafer, Alan Wayne
TITLE OF INVENTION: DETECTION OF A LEPTIN RECEPTOR
TITLE OF INVENTION: VARIANT AND METHODS FOR REGULATING
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of The Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ Version 2.0
CURRENT APPLICATION NUMBER: US/08/588,190
FILLING DATE: 18-JAN-1996
CLASSIFICATION ONTA:
APPLICATION HOMBER: US/08/588,190
FILING DATE: 18-JAN-1996
CLASSIFICATION NUMBER: US/08/588,190
FILING DATE: 18-JAN-1996
CLASSIFICATION NUMBER: US/08/588,190
FILING DATE: 18-JAN-1996
CLASSIFICATION NUMBER: US/08/588,190
FILING DATE: 18-JAN-1996
CLASSIFICATION NUMBER: US/08/588,190
FILING DATE: 18-JAN-1996
CLASSIFICATION HOMBER: US/08/588,190
FILING DATE: 18-JAN-1996
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FILING DATE: 18-JAN-1996
CLASSIFICATION NUMBER: US/08/588,190
FILING DATE: APPLICATION HOMBER: US/08/588,190
FILING DATE: APPLICATION HOMBER: US/08/588,190
FILING DATE: 18-JAN-1996
CLASSIFICATION NUMBER: US/08/588,190
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US-08-588-190-3
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                                                               QDDIEKHQSDAGLYVIVPVIISSSILLIGTL
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                                                                                                                                                                                                                                                   SLYCSDIPSIHPISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCV SLYCSDIPSIHPISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCV
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                                                                                                                                                        NGDTMKKEKNVTLLWKPLMKNDSLCSVQRYV.
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LPDSVVKPLPPSSVKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVY
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Sequence 3, Application Patent No. 6355237 GENERAL INFORMATION:

US/08618957A

APPLICANT:
APPLICANT:
APPLICANT:

Snodgrass, H. R Cioffi, Joseph Zupancic, Thoma

Ralph

Joel

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; MOLECULE TYPE: US-08-618-957A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Poissant, Brian M.

REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 0089(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
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APPLICATION NUMBER: US/08/618,957A
FILING DATE: 20-MAR-1996
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CITY: N
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OPERATING SYSTEM:
SOFTWARE: FastSE
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mes 780; Conser
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                                                  FHCIYKKENKIVPSKEIVWWMNLAEKIPQSQYDVVSDHVSKVTFFNLNETKPRGKFTYDA
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SLYCSDIPSIHPISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCV
SLYCSDIPSIHPISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCV
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SEE: Pennie & Edmonds LLP
1: 1155 Avenue of The Ameri
New York
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US-08-588-526-3
; Sequence 3, Application
. Patent No. 5882860
                             REFERENCE/DOCKET NUMBER: 8907
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 908 amino acids
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                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
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APPLICANT:
                                                                                                                                                                APPLICATION NUMBER: US/08 FILING DATE: 18-JAN-1996 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Poissant, Brian M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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TOPOLOGY: li
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STREET: 11
CITY: New
                                                                                                                                                   NAME: Poissant, Brian REGISTRATION NUMBER: :
                                                                                                                                                                                                                                                                                                                                                           STATE: New York
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LPDSVVKPLPPSSVKAEITINIGLLKISWEKPVFPENNLQFQIRYGLSGKEVQWKMYEVY 591
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Shafer, Alan
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Cioffi, Jo
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18-JAN-1996
JN: 435
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c, Thomas
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RESULT 17
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Best Local S
Matches 774
                                                                               Sequence 11, Application US/08640389A Patent No. 5912123
GENERAL INFORMATION:
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: DETECTION OF THE LEPTIN
TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS
TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY
NUMBER OF SEQUENCES: 16
                                             APPLICANT: Snodgrass, H. APPLICANT: Cloffi, Joseph APPLICANT: Zupancic, Thon Applicant: Shafer, Alan L
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                                                  Joseph
C, Thomas
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REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
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Best Local Similarity
Matches 970; Conser
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,389/
FILING DATE: 29-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: POISSANT, Brian M.
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TOPOLOGY: unk
MOLECULE TYPE:
8-640-389A-11
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CITY: New YOUR STATE: New YOUR COUNTRY: USA
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RESULT 18
US-08-306-231-3
; Sequence 3, Application
; Patent No. 5643748
; GENERAL INFORMATION:
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                                                                                                                                           ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the America:
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VG
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,231
FILING DATE: 14-SEP-1994
CLASSIFICATION: 435
TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 569 amino acids
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7225-076
TELECOMMUNICATION INFORMATION:
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                                                   TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
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Cioffi, Joseph
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RESULT 19
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; TOPOLOGY: linear
; MOLECULE TYPE: pro
US-08-306-231-3
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Best Local S
Matches 459
                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                        Sequence
       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,389A
FILING DATE: 29-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                   APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: DETECTI
TITLE OF INVENTION: RECEPTO
TITLE OF INVENTION: REGULAT
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
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CITY: 1
                                                                                                                            STATE: New York
COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                       STATE:
                                                                                                                                                                                               ADDRESSEE:
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459; Conser
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                                                                                                                                                                     New York
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Pred. No
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N REPRODUCTIVE ORGANS AND METHODS FOR REPRODUCTIVE BIOLOGY
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RESULT 20
US-08-640-389A-9
; Sequence 9, Application U
; Patent No. 5912123
; GENERAL INFORMATION:
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; TOPOLOGY: unk
; MOLECULE TYPE:
US-08-640-389A-10
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REFERENCE/DOCKET NUMBER: 8907-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 896 amino acids
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Best Local Similarity 99.5%;
Matches 607; Conservative
APPLICANT:
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Snodgrass, H. Cioffi, Joseph
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; TOPOLOGY: un; MOLECULE TYPE: US-08-640-389A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ver

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/640,389A

FILING DATE: 29-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: POISSANT, Brian M.

REGISTRATION NUMBER: 28,462

REFERENCE/DOCKET NUMBER: 8907-032

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 906 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 607; Conserv
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APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: DETECTION OF THE LEPTIN
TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1155 Ave
CITY: New York
STATE: New York
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ZIP: 10036-2
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                                                                                                                                                                                                                                                                                                                                                                                                           READKIVSATSLLVDSILPGSSYEVQVRGKRLDGPGIWSDWSTPRVFTTQDVIYFPPKIL 341
                GPEFWRIINGDTMKKEKNVTLLWKPLMKNDS:
                                                                 QWKMYEYYDAKSKSVSLPVPDLCAVYAVQVRCKRLDGLGYWSNWSNPAYTVVMDIKVPMR 641
                                                                                                                                  LDSPPTCVLPDSVVKPLPPSSVKAEITINIG
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99.5%;
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Pred.
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LCSVQRYVINHHTSCNGTWSEDVGNHTKF 701
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                CSVQRYVINHHTSCNGTWSEDVGNHTKF 701
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3.8e-301;
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RESULT 21
US-08-640-389A-8
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,389A
FILING DATE: 29-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-032
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                      Matches
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TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SAPPLICANT:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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STREET: 1155 Aver
CITY: New York
STATE: New York
COUNTRY: USA
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TOPOLOGY: un
                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                     READKIVSATSLLVDSILPGSSYEVQVRGKRLDGPGIWSDWSTPRVFTTQDVIYFPPKIL 341
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10036-2711
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1155 Avenue
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Cloffi, Joseph
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                                                                                                                                                                                      Score 307; DB 2;
Pred. No. 4e-301;
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                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                            Length 958;
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US-08-803-346-64
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                                                                                                                                                                                                                                            ZIP: 07065

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compati
OPERATING SYSTEM: DOS
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APPLICANT:
                                                                                                                                     SOFTWARE: FastSEQ for Windows Ver: CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,346
FILING DATE: 20-FEB-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: PHILLIPS, MICHAEL SEAN TITLE OF INVENTION: RAT OB RECEPTORS TITLE OF INVENTION: ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: JOANNE M. GIESSER - 1
STREET: 126 EAST LINCOLN AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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882 SWAQGLNFQK 891
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STATE: NJ
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LDSPPTCVLPDSVVKPLPPSSVKAEITINTGLLKISWEKPVFPENNLQFQIRYGLSGKEV 581
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LIU, QINGYUN
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Best Local Similarity
77; Conserv
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Sequence 61, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HESS, JOHN W.
APPLICANT: CASKEY, C. THOMAS
APPLICANT: LIU, QINGYUN
APPLICANT: PHILLIPS, MICHAEL SEAN
TITLE OF INVENTION: RAT OB RECEPTOR:
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 77
                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,346
FILING DATE: 20-FEB-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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TELEPHONE: 732-594-3046
TELEFAX: 732-594-4720
                                                                                                      REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3046
TELEFAX: 732-594-4720
                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: GIESSER, JOANNE M
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOANNE M.
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           STRANDEDNESS:
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ZIP: 07065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                           amino acid
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                                           76 amino acids
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llarity 100.0%;
Conservative
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linear
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          single
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RAT OB RECEPTORS AND NUCLEOTIDES
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Pred. No.
                                                                                                                                                     .9642Y
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Sequence 2, pr
; Sequence 2, pr
; Patent No. 5972621
; Patent No. Tartagl
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US-08-599-455B-2
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                                                                                                                                                                                            APPLICATION NUMBER: US/08/599,45:
FILING DATE: 22-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L
                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                      REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Culpepper, TITLE OF INVENTION: MITTLE OF INVENTION: MINUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                             TYPE:
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                                                                                                          TELEPHONE: 617-542-8906
                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
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ZIP: 02110-2804
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                                                          LENGTH:
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mino acid
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225 Franklin
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Conservative
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                               linear
protein
internal
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Pred. N
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DDY WEIGHT USING THE OB RECEPTOR
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Query Match

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DB 2;

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Tartagl
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US-09-069-781B-2
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Matches
                                                                                  TELEX: 200154
INFORMATION FOR SEQ ID NO:
MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FASTSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                          FILING DATE: 28-MAY-1997
APPLICATION NUMBER: US 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: US 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: US 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: US 08/583,153
APPLICATION NUMBER: US 08/583,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 29-APRI PRIOR APPLICATION DATA:
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                                                                      SEQUENCE
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                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/569,485 FILING DATE: 08-DEC-1995 FILING DATE: 08-DEC-1995
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                                                                                                                                                                                       NAME:
                                                                                                                                                                                                          APPLICATION NUMBER: US 08/565,622 FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/562,663 FILING DATE: 27-NOV-1995
                           TYPE: amino acid
TOPOLOGY: unknow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                             TELEPHONE:
                                                                                                                                                        REFERENCE/DOCKET NUMBER: 35
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5, 6287782
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                                                                   CHARACTERISTICS:
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E: Fish & Richardson,
225 Franklin Street
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                                                                                                              (617) 542-5070
(617) 542-8906
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JMBER: US 08/570,142
11-DEC-1995
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US-08-618-957A-12
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; MOLECULE TYPE:
US-08-618-957A-12
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Patent No.
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RESULT 27
US-08-827-962-19
; Sequence 19, Application US/08827962A
; Patent No. 6258944
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                               TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: 650-493-4935
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                                                                                 498 FOPIFLLSGYTMWIRINHSLGSLDSPPTCVLPD:
                                                                                                                                                                                                                                                                                                                                          NAME: Poissant, Brian REGISTRATION NUMBER: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
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                                                                                                                                 Similarity 42; Conserv
                                                                                                                                                                                                                                                                    E CHARACTERISTICS
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6355237
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                                                                                                                                                                                                                                           amino acid
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1155 Avenue of The Americas
                                                                                                                                                                                                                                                                                                         650-493-5556
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                                                                                                                                  Conservative
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Pred. No.
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Pred. No.
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Mismatches 0; Indels
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RESULT 29
US-08-640-389A-12
; Sequence 12, App
; Patent No. 59121
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PRIOR FILING DATE: 1996-05-06;
NUMBER OF SEQ ID NOS: 21;
SOFTWARE: FastSEQ for Windows Version 4.0;
SEQ ID NO 19;
LENGTH: 895;
TYPE: PRT;
ORGANISM: Rattus No. 6258944vegicus
US-08-827-962-19
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US-08-827-962-21
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SEQ ID NO 21
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TITLE OF INVENTION: C
TITLE OF INVENTION: E
FILE REFERENCE: 19693
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Best Local Similarity
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Best Local
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CURRENT APPLICATION NUMBER: US/08/827,962A
CURRENT FILING DATE: 1997-05-06
                                                                                                                                            GENERAL INFORMATION:
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PRIOR FILING DATE: 1996-05-06
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                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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                                                APPLICANT: Zupancic, Thoma APPLICANT: Shafer, Alan W. TITLE OF INVENTION: DETECT TITLE OF INVENTION: REGULA
                        CORRESPONDENCE ADDRESS:
                                                                                                                   APPLICANT:
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1 Similarity 100.0%;
42; Conservative
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WENTION: OB RECEPTOR ISOFORMS
                                     SEQUENCES:
: Pennie & 1155 Avenue
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Cioffi, Josep
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larity 100.0%;
Conservative
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N: OB RECEPTOR ISOFORMS AND NUCLEIC ACIDS
N: ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                  No. 6258944vegicus
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                                                                                                                   Joseph
                                                  REGULATING
                                                               DETECTION OF THE LEPTIN RECEPTOR IN REPRODUCTIVE
                                                                                                    Thomas J.
                                      16
Edmonds of the F
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Pred. No.
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Pred. No
Americas
                                                 REPRODUCTIVE
                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                     DB
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEIC
                                                  E ORGANS
BIOLOGY
                                                                                                                                                                                                                                                                                                               Length 895;
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                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 43, Application Patent No. 5972621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                      STREET: 222
STREET: 222
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,38
FILING DATE: 29-APR-1996
FILING DATE: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                 SOFTWARE: FASTSEQ for Windows CURRENT APPLICATION DATA; APPLICATION NUMBER: US/08/599, FILING DATE: 22-JAN-1996
                                                                                                                                                                                                                      COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/5;

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: 08/5;

FILING DATE: 11-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: POISSANT, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Culpepper, TITLE OF INVENTION: M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                       COMPUTER: IBM Compatible OPERATING SYSTEM: Windows
APPLICATION NUMBER: 08/569,485 FILING DATE: 08-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 3.6%;
l Similarity 100.0%;
42; Conservative
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(212) 869-9741/8864
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                                                                                   08/583,153
                                                  08/570,142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Louis A.
                                                                                                                                       US/08/599,455E
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                                                                                                                                                                          Version 2.0
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No. 1.4e-33;
atches 0; Indels
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APPLICATION NUMBER:

08/566,622

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RESULT 31
US-08-827-962-15
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; ORGANISM: Rattus
US-08-827-962-15
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Best Local Similarity 100.0%;
Matches 42; Conservative (
                                                                                         Sequence 20, Application US/08827962A Patent No. 6258944 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/08827962A Patent No. 6258944
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                          Matches
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SEQ ID NO 15
LENGTH: 1162
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PRIOR FILING DATE: 1996-05-06
NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/08/827,962A CURRENT FILING DATE: 1997-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MERCK F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 617-542-50:
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
FILE REFERENCE: 19693
CURRENT APPLICATION NUMBER: US/08/827,962A
CURRENT FILING DATE: 1997-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 196
                                            APPLICANT: MERCK & CO., INC.
TITLE OF INVENTION: OB RECEPTOR ISOFORMS AND NUCLEIC
TITLE OF INVENTION: ENCODING THEM
                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
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LENGTH: 1162 amino acids
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                                                                                                                                                                                                           498 FQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPPS 539
                                                                                                                                                                                                                              500 FQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPPS 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPPS 539
                                                                                                                                                                                                                                                                            42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MERCK & CO., INC.
VENTION: OB RECEPTOR ISOFORMS AND NUCLEIC
                                                                                                                                                                                                                                                                           Conservative
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19693
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R: 35,283
UMBER: 07334/017001
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100.0%;
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                                                                                                                                                                                                                                                                        Score 42; DB; Pred. No. 1.7; Pred. No. 1.7
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                                                                                                                                                                                                                                                                                          DB 4; L
1.7e-33;
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                                                     ; TOPOLOGY: 1; MOLECULE TYPE: US-08-803-346-1
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US-08-803-346-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Rattus No. US-08-827-962-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
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 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM COMPONERTING SYSTEM:
SOFTWARE: FastSEQ
CURRENT APPLICATION I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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                                                                                                                                                                                       REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3046
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/803,346
FILING DATE: 20-FEB-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: GIESSER, JOANNE M
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                          TYPE: amino STRANDEDNESS:
                                                                                                                                                                TELEPHONE: 732-33-4720
                                                                                                                                                               TELEX:
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5. 6281346
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  Similarity
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                                                                                                                       1162
                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                         IBM Compatible
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                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOANNE M. GIESSER - MERCK & CO., INC 6 EAST LINCOLN AVENUE - P.O. BOX 2000
                                                                  protein
                                                                                          single
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 3.6%;
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RAT OB RECEPTORS
ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                DOS
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Pred. No. 1.7e-33;
0; Mismatches 0; Indels
             Score 42;
   Pred.
                                                                                                                                                                                                                                                                                                                                                                 Version 2.0
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DB 4; Length 1162; 1.7e-33;
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US-09-069-781B-43
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                                                                                                                                                                                     APPLICATION NUMBER: US US, APPLICATION NUMBER: US US, FILING DATE: 04-DEC-1995
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/082/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
                    Query Match
Best Local
        Matches
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GENERAL INFORMATION:
                                                                                                                                                                                    TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/9
FILING DATE: 22-JAN-1996
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: US 08/9
TITTUG DATE: 28-DEC-1995
TITTUG DATE: 115 08/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 29-APRI PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
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FILING DATE: 28-MAY-1997
APPLICATION NUMBER: US 08/708,123
FILING DATE: 03-SEP-1996
FILING DATE: US 08/638,524
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STATE:
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THE DATE: 11-DEC-1995

THE DATE: 11-DEC-1995
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FILING DATE: 29-APRIL-1998
                                                                                                                                       TOPOLOGY:
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     . Similarity 42; Conserv
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larity 100.0%;
Conservative
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Tepper, Robert I.
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                                                                                                       protein
internal
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                    Score 42;
Pred. No
    ed. No. 1. Mismatches
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RESULT 36
US-08-701-382-6
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US-08-803-346-63
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Matches
                                                 Sequence 6, Application US/08701382 Patent No. 6004758 GENERAL INFORMATION:
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                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Ve CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,34
FILING DATE: 20-FEB-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: CIESCED TOWNEY
                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                NAME: GIESSER, JOANNE M
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 1964
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3046
TELEFAX: 732-594-4720
 TITLE OF
                          APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOANNE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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STREET: LL.
TTTY: RAHWAY
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STRANDEDNESS: si
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INVENTION:
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EAST LINCOLN AVENUE
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RECEPTOR DERIVED
MODULATION OF RE
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Pred.
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red. No. 2.2e-16;
Mismatches 0; Indels
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P.O. BOX 2000
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RESULT 37
US-09-028-937-6
; Sequence 6, Application U
; Patent No. 6333031
; GENERAL INFORMATION:
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Best Local
                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Vo

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/028,937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-494-8771
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: SHERWOOD, Pamela J.
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: A631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-8771
TELEFAX: 415-494-8771
                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/788,820
FILING DATE: 23-JAN-1997
                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: doul
TOPOLOGY: linear
HOLECULE TYPE: prot
                                                                                                                                                                                                       STREET: .
                                                                                                                                                                                                                           ADDRESSEE:
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                                         FILING DATE: CLASSIFICATION:
                                                                                                                                                                     COUNTRY: USA
ZIP: 94111-4187
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les 23; Conserv
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941114187
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CA
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4 Embarcadero Center,
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larity 100.0%;
Conservative
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Embarcadero Cent
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; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 23-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 08-MAR-1996
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/701,382
FILING DATE: 22-AUG-1996
                                                                                                                                                                                                NAME: Trecartin, Richard F. REGISTRATION NUMBER: 31,801 REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1. CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,
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MEDIUM TYPE: Floppy |
COMPUTER: IBM PC com
OPERATING SYSTEM: PC
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ATTORNEY/AGENT INFORMATION:
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TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
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23; Conserv
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(415) 781-1989
(415) 398-3249
910 277299
FOR SEQ ID NO
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Floppy disk
BM PC compatible
STEM: PC-DOS/MS-DOS
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23-JAN-1997
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08-MAR-1996
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a, Tatjana
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; FEATURE:
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US-08-788-820-6
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Best Local :
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Best Local
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                                                                                                                                                         INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: GIESSER, JOANNE M
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 1964
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3046
                                                                                                                                                                                                                                                                        FILING DATE: 20-FEB-19
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                      ***CTERISTICS:

77 amino acids

****rPE: amino acid

STRANDEDNESS: s'

TOPOLOGY:

OLECULF '
                                                                                                                                 SEQUENCE CHARACTERISTICS: LENGTH: 77 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOANNE M. GIESSER - N
STREET: 126 EAST LINCOLN AVENUE
                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: US/08/803,346
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OPERATING SYSTEM:
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les 23; Conser
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ZIP: 07065
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STRANDEDNESS: uni
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LIU, QINGYUN
PHILLIPS, MIC
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20-FEB-1997
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RAT OB RECEPTORS AND NUCLEOTIDES
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19642Y
             Score 20;
Pred. No.
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Pred. No.
   Mismatches
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DB 4; L., 2.4e-12; 0;
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s 0;
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; TOPOLOGY: ur
; MOLECULE TYPE:
US-08-306-231-14
                                                                                                                 US-08-306-231-15; Sequence 15, Application US/08306231; Patent No. 5643748; GENERAL INFORMATION:
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US-08-306-231-14
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                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches: 15; Conserv
APPLICANT: CLUBANCIC, Thomas J.
APPLICANT: Supancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A
TITLE OF INVENTION: RECEPTOR
TITLE OF SECHENCES: 15
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                                                                                   APPLICANT: APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                              301 GSSYEVQVRGKRLDG 315
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REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
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5643748
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1155 Avenue of the
                                                                                   Snodgrass, H. Cioffi, Josep
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                                       NOVEL HEMATOPOIETIN
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RESULT 42
US-08-355-888A-30
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 72
TELECOMMUNICATION INFORMATION:
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                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/355,88
                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                        TITLE OF INVENTION:
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ADDRESSEE: Pennie & Edmonds
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CLASSIFICATION: 435
 CLASSIFICATION: 435
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TELEFAX: (212) 8
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10036-2711
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New York
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INFORMATION:
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c, Thomas J.
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RECEPTOR
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; TOPOLOGY: u; MOLECULE TYPE: US-08-355-888A-31
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Best Local Similarity
Matches 15; Conserv
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/355,888A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
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                                                                                                                                                    TELEFAX: (212) 869-97
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 72
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Poissant, Brian M. REGISTRATION NUMBER: 28,
                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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o. 5763211
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                                                                                   unknown
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12) 869-9741/8864
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RECEPTOR
31
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1.3%;
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R: 7225-078
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                                                                                                                                                                                                                                                                                                                                       Version #1.30
; DB 1; Length 15;
5.5.9e-08;
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Matches

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; STRANDEDNESS:
; TOPOLOGY: unk
; MOLECULE TYPE:
US-08-693-697-30
                                                                                                                                               RESULT 45
US-08-693-697-31
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US-08-693-697-30
                                                                                            Patent No. 5869610
GENERAL INFORMATION:
                                                                                                              Sequence 31, Application US/08693697 Patent No. 5869610
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 15; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 05-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
OPERATING SYSTEM: PC-DOS,
SOFTWARE: FastSEQ for Wi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,697
                                                                               APPLICANT:
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CORRESPONDENCE ADDRESS:
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ZIP: 10036-2711
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). 5869610
             NT: Snodgrass, H. R.
NT: Cioffi, Joseph
NT: Zupancic, Thomas J.
NT: Shafer, Alan W.
F INVENTION: Hu-Bl.219, 1
                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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Shafer, Alan W.
Shafer, Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
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                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                          unknown
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                NOVEL HUMAN HEMATOPOIETIN
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US-08-693-696-30
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
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Best Local
                                                         COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ for Windows Va
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/593,69
FILING DATE: 05-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
                                                                                                                                                                                  STREET: 1155 Avenue of the Am CITY: New York
STATE: New V-
                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                       APPLICANT: Shafer, Alan TITLE OF INVENTION: Hu-E TITLE OF INVENTION: RECE NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
TOR APPLICATION DATA:
                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CAVYAVQVRCKRLDG 15
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15; Conser
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.us/08/693,697
.05-AUG-1996
.ON: 435
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for Windows Ver
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                                               us/08/693,696
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                                                                            Version #1.30
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US-08-693-696-31
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REFERENCE/DOCKET NUMBER: 7225-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                            NAME: POISSANT, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7225-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 15; Conserv
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Shafer, Alan W. TITLE OF INVENTION: Hu-B1.219, TITLE OF INVENTION: RECEPTOR NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/693,696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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TYPE: amino STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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10036-2711
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Zupancic,
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llarity 100.0%;
Conservative
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                                                                                                                                                                                                                             US 08/355,888
                                                                                                                                             28,462
BER: 7225-078
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Pred. No.
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5.9e-08;
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RESULT 49
US-08-355-888A-25
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; MOLECULE TYPE:
US-08-693-696-31
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US-08-306-231-9
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                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,231
FILING DATE: 14-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: POISSANT, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7225-076
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
I-PURCH 13 Amino acids
Sequence 25 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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                                                                               604 CAVYAVQVRCKRLDG 618
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                                                                                                                                       Local Similarity
les 13; Conserv
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TOPOLOGY: ur
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5. 5643748
 25, Application US/08355888A
5, 5763211
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                                                                                                                                       Conservative
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Cioffi, Joseph
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E: peptide
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Pred.
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Mismatches 0; Indels
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STRANDEDNESS:

TOPOLOGY: unb

MOLECULE TYPE:

US-08-355-888A-25
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; Sequence 25, Ap
; Patent No. 5869
                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: POISSANT, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7225-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 100.
13; Conservative
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WF
SOFTWARE: Paten+**
CURRENT ****
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APPLICANT: Snodgr
APPLICANT: Cioffi
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the /
CITY: New York
                                                                                                                                                                   APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219,
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/355,888A FILING DATE: 14-DEC-1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                             STATE: N
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1: 1155 Avenue of the Americas
New York
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amino acid
                                                                             New York
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                                                             USA
                                                                                                                                                                                                                               Snodgrass, H. Cioffi, Josep
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Cloffi, Jo
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Lc, Thomas J.
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Search completed: May 18, 2002, 07:04:11 Job time: 290 sec
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                                                                                                                                                                                                                                                                                                            NAME: POISSANT, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
                                                                                                                                                        Query Match 1.1%;
Best Local Similarity 100.0%;
Matches 13; Conservative
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SOFTWARE: FastSEQ for Windows Ver
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                                                    569 QFQIRYGLSGKEV 581
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1 QFQIRYGLSGKEV 13
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E: peptide
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BER: 8907-003
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